

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 24, 2004, 02:09:41 ; Search time 65 Seconds
(without alignments)
1344.593 Million cell updates/sec

file: US-09-600-932-2

effect score: 1484

sequence: 1 MNGFASLLRNQFILLVFL.....NDTECHLTMYFVCFIKKK 277

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1017041 seqs, 315518202 residues

total number of hits satisfying chosen parameters: 1017041

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database :

SPTREMBL_25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeo:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1484	100.0	277	Q9Y6Z7	Q9Y6Z7 homo sapien
2	1330	89.6	277	Q8C1C5	Q8C1C5 mus musculus
3	1327	89.4	277	Q8CF98	Q8CF98 mus musculus
4	734	49.5	271	Q7T0T0	Q7T0T0 xenopus lae
5	728	49.1	272	Q9DC75	Q9DC75 mus musculus
6	716.5	48.3	271	Q9BWP8	Q9BWP8 homo sapien
7	634	42.7	268	Q7Z6N1	Q7Z6N1 homo sapien
8	344.5	23.2	369	Q863A1	Q863A1 bos taurus
9	338.5	22.8	378	Q9N1X4	Q9N1X4 sus scrofa
10	337	22.7	254	Q98TA4	Q98TA4 gallus gall
11	337	22.7	375	Q86YK9	Q86YK9 homo sapien
12	334.5	22.5	251	Q919Q8	Q919Q8 brachydanio
13	333	22.4	375	Q8TCD8	Q8TCD8 homo sapien
14	327.5	22.1	238	Q574S1	Q574S1 gallus gall
15	316	21.3	256	Q919Q9	Q919Q9 cyprinus ca
16	307	20.7	246	Q919Q7	Q919Q7 carassius a

ALIGNMENTS

RESULT 1

Q9Y6Z7 PRELIMINARY; PRT; 277 AA.
ID Q9Y6Z7
AC Q9Y6Z7
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Collectin 34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99240768; PubMed=10224141;
RA Ohtani K., Suzuki Y., Eda S., Kawai T., Kase T., Yamazaki H.,
RA Keshi H., Sakai Y., Fukuchi A., Sakamoto T., Wakamiya N.;
RT "Molecular cloning of a novel collectin from liver (CL-Li).";
RL J. Biol. Chem. 274:13681-13689 (1999).
DR EMBL; AB002631; BAA81747.1;
DR HSP; P19999; 2MSB.
DR Genew; HGNC:2220; COLEC10.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00441; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 277 AA; 30733 MW; 9736861CBED5C25 CRC64;

Query Match 100.0%; Score 1484; DB 4; Length 277;
Best Local Similarity 100.0%; Pred.No. 2.6e-129;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRNQFILLVFLQISLGLDIDSRPAEYCATHTISPGPKGDDGKDPGE 60

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Db 1 MNGFASLLRRNQIFLLVFLQIQLSLGLDIDSRPTAEVCATHTISPGPKDDGKGDGPE 60
61 EGKHKVGRMGPKGIKGLGDMGDRGNIGKTGPIGKKGDKGKGLLIGPGEKAGTVCVD 120
61 EGKHKVGRMGPKGIKGLGDMGDRGNIGKTGPIGKKGDKGKGLLIGPGEKAGTVCVD 120
121 CGRYKRVGQDLSIARLKTSMKFKVKNVIAGIRETEKEFYIIVQEEKNYRESLTHCRIRG 180
121 CGRYKRVGQDLSIARLKTSMKFKVKNVIAGIRETEKEFYIIVQEEKNYRESLTHCRIRG 180
181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVLEREGQYFMTDNTPLQYNNWNEGEPS 240
181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVLEREGQYFMTDNTPLQYNNWNEGEPS 240
241 DPYGHEDCVEMLSGRNDTECHLTMFVCFEYFKKKK 277
241 DPYGHEDCVEMLSGRNDTECHLTMFVCFEYFKKKK 277

RESULT 2
28C1C5 PRELIMINARY; PRT; 277 AA.
ID Q8C1C5
AC Q8C1C5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin 34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK028423; BAC25941.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30510 MW; 94EF23A2E5404872 CRC64;

Query Match 89.6%; Score 1330; DB 11; Length 277;
Best Local Similarity 88.8%; Pred. No. 4.9e-115;
Matches 246; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQIFLLVFLQIQLSLGLDIDSRPTAEVCATHTISPGPKDDGKGDGPE 60
Db 1 MNGFVLLRSNLMLLVLALLHFQSLGLVDVSRGAEVCATHTISPGKDDGGERDGTGE 60
QY 61 EGKHKVGRMGPKGIKGLGDMGDRGNIGKTGPIGKKGDKGKGLLIGPGEKAGTVCVD 120
Db 61 EGKDKVGRQGPVKGVKGLGDMGAQGNIGKSGPIGKKGDKGKGLLIGPGEKAGTICD 120
QY 121 CGRYKRVGQDLSIARLKTSMKFKVKNVIAGIRETEKEFYIIVQEEKNYRESLTHCRIRG 180
Db 121 CGRYKRVGQDLSIARLKTSMKFKVKNVIAGIRETEKEFYIIVQEEKNYRESLTHCRIRG 180
QY 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVLEREGQYFMTDNTPLQYNNWNEGEPS 240
Db 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVLEREGQYFMTDNTPLQYNNWNEGEPS 240
241 DPYGHEDCVEMLSGRNDTECHLTMFVCFEYFKKKK 277
241 DPYGHEDCVEMLSGRNDTECHLTMFVCFEYFKKKK 277

RESULT 4
Q7T0T0 PRELIMINARY; PRT; 271 AA.
ID Q7T0T0
AC Q7T0T0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
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Db 241 DPSGHEDCVEMLSGRNDTECHLTMFVCFEYFKKKK 277

RESULT 3
Q8CF98 PRELIMINARY; PRT; 277 AA.
ID Q8CF98
AC Q8CF98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin-L1. (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22333927; PubMed=12450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA Fukuoh A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL Biosci. Biotechnol. Biochem. 66:2134-2145(2002).
DR EMBL; AB016429; BAC53954.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30524 MW; 98C743A2E07A2872 CRC64;

Query Match 89.4%; Score 1327; DB 11; Length 277;
Best Local Similarity 88.4%; Pred. No. 9.2e-115;
Matches 245; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQIFLLVFLQIQLSLGLDIDSRPTAEVCATHTISPGPKDDGKGDGPE 60
Db 1 MNGFVLLRSNLMLLVLALLHFQSLGLVDVSRGAEVCATHTISPGKDDGGERDGTGE 60
QY 61 EGKHKVGRMGPKGIKGLGDMGDRGNIGKTGPIGKKGDKGKGLLIGPGEKAGTVCVD 120
Db 61 EGKDKVGRQGPVKGVKGLGDMGAQGNIGKSGPIGKKGDKGKGLLIGPGEKAGTICD 120
QY 121 CGRYKRVGQDLSIARLKTSMKFKVKNVIAGIRETEKEFYIIVQEEKNYRESLTHCRIRG 180
Db 121 CGRYKRVGQDLSIARLKTSMKFKVKNVIAGIRETEKEFYIIVQEEKNYRESLTHCRIRG 180
QY 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVLEREGQYFMTDNTPLQYNNWNEGEPS 240
Db 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVLEREGQYFMTDNTPLQYNNWNEGEPS 240
241 DPYGHEDCVEMLSGRNDTECHLTMFVCFEYFKKKK 277
241 DPYGHEDCVEMLSGRNDTECHLTMFVCFEYFKKKK 277

RESULT 4
Q7T0T0 PRELIMINARY; PRT; 271 AA.
ID Q7T0T0
AC Q7T0T0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
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{ Pfam; PF01391; Collagen; 3.
{ Pfam; PF00059; lectin c; 1.
{ SMART; SM00034; CLECT; 1.
{ PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
{ PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
{ SIGNAL.
{ CHAIN 1 20 Potential.
{ CHAIN 21 67 surfactant protein D.
{ CHAIN 245 369 surfactant protein D.
{ SEQUENCE 369 AA; 37405 MW; 4A74B7593508A5D CRC64;

Query Match 23.2%; Score 344.5; DB 6; Length 369;
Best Local Similarity 29.7%; Pred. No. 1.7e-23;
Matches 88; Conservative 38; Mismatches 111; Indels 59; Gaps 8;

26 LGLDSDSPTAEVCATHISIPGKGDDEKGP-----GEGKHGKVGMRGPKIGKEL 79
84 IGLKDNDSAGE-----GPKGDTGPPGMPGPGAGREGSGKSGMGPPTGPK 135
80 GDMGRGNI-----GKTGPIGKKDKOE----- 102
136 GDTGPKGVGAPGIQSPGAPGLKGERGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 195
103 --KGLLGPGEKAGT--VDCGYRKFVGLDISIARLKTSMKFKV--VIAGIRETE 156
196 GLKGRGTPGERGAGGESGLAEVNALRORVILLEGQQLRQNLQAFSQYKXKMLFPNGRSVG 255
157 EKFYIVQEKYRSLTHCRIRGMLAMPKDEAAANTLIADYVAKSGFFRFFVGVNDLER 216
256 EKIFTEGSEKTFQDAQICTQAGQLSPRSAAENEALTQ-LATAQKAAFLSMSDTRK 314
217 EQGYMFTDNTPLQNTYNNNEGPPDPYGHEDCVEMLSGRWNTDECHLTMYFVCEP 272
315 EGTFTYPTGEPLV-YSNWAPGPNNDGSENCVEIFPNKGKNDKVCGEQRLVICEF 369

RESULT 9
9N1X4 PRELIMINARY; PRT; 378 AA.
C Q9N1X4;
I 01-OCT-2000 (TrEMBLrel. 15, Created)
T 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
E 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E Lung surfactant protein D precursor.
N SFTPD.
S Sus scrofa (Pig).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
X NCBI_TaxID=9823;
P [1]
N P SEQUENCE FROM N.A.
X MEDLINE=20109098; PubMed=10640760;
A van Eijk M., Haagsman H.P., Skinner T., Archibald A.L., Reid K.B.M.,
L Lawson P.R.;
T "Porcine Lung Surfactant Protein D (SP-D): cDNA cloning, chromosomal
localisation and tissue distribution.";
L J. Immunol. 164:1442-1450(2000).
L EMBL; AF132496; AAF22145.2; -
R HSP; P35247; 1B08
R GO; GO:0005529; P:sugar binding; IEA.
R InterPro; IPR008161; C1g_helix.
R InterPro; IPR008160; Collagen.
R InterPro; IPR001304; Lectin C.
R Pfam; PF00059; Lectin c; 1.
R Pfam; PF00059; Lectin c; 1.
R ProDom; PD000007; C1g_helix; 2.
R SMART; SM00034; CLECT; 1.
R PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
R PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
R Collagen; Signal.
T SIGNAL 1 20 POTENTIAL.
T CHAIN 21 378 LUNG SURFACTANT PROTEIN D.
T SEQUENCE 378 AA; 37986 MW; 3504E8C1E56C341D CRC64;

{ Pfam; PF01391; Collagen; 3.
{ Pfam; PF00059; lectin c; 1.
{ SMART; SM00034; CLECT; 1.
{ PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
{ PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
{ SIGNAL.
{ CHAIN 1 20 Potential.
{ CHAIN 21 67 surfactant protein D.
{ CHAIN 245 369 surfactant protein D.
{ SEQUENCE 369 AA; 37405 MW; 4A74B7593508A5D CRC64;

Query Match 23.2%; Score 344.5; DB 6; Length 369;
Best Local Similarity 29.7%; Pred. No. 1.7e-23;
Matches 88; Conservative 38; Mismatches 111; Indels 59; Gaps 8;

26 LGLDSDSPTAEVCATHISIPGKGDDEKGP-----GEGKHGKVGMRGPKIGKEL 79
84 IGLKDNDSAGE-----GPKGDTGPPGMPGPGAGREGSGKSGMGPPTGPK 135
80 GDMGRGNI-----GKTGPIGKKDKOE----- 102
136 GDTGPKGVGAPGIQSPGAPGLKGERGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 195
103 --KGLLGPGEKAGT--VDCGYRKFVGLDISIARLKTSMKFKV--VIAGIRETE 156
196 GLKGRGTPGERGAGGESGLAEVNALRORVILLEGQQLRQNLQAFSQYKXKMLFPNGRSVG 255
157 EKFYIVQEKYRSLTHCRIRGMLAMPKDEAAANTLIADYVAKSGFFRFFVGVNDLER 216
256 EKIFTEGSEKTFQDAQICTQAGQLSPRSAAENEALTQ-LATAQKAAFLSMSDTRK 314
217 EQGYMFTDNTPLQNTYNNNEGPPDPYGHEDCVEMLSGRWNTDECHLTMYFVCEP 272
315 EGTFTYPTGEPLV-YSNWAPGPNNDGSENCVEIFPNKGKNDKVCGEQRLVICEF 369

RESULT 10
Q99TA4 PRELIMINARY; PRT; 254 AA.
AC Q98TA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mannose-binding lectin protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20456722; PubMed=1100389;
RA Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjoldt K.;
RT "The homologue of mannose-binding lectin in the carp family Cyprinidae
is expressed at high level in spleen, and the deduced primary
structure predicts affinity for galactose.";
RL Immunogenetics 51:955-964(2000).
DR EMBL; AF231714; AAK30298.1; -
DR HSP; P19999; 1YTT.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005529; P:sugar binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008161; C1g_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR ProDom; PD000007; C1g_helix; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
KW Collagen; Lectin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 254 MANNOSE-BINDING LECTIN PROTEIN.
FT VARIANT 234 234 D -> V.
SQ SEQUENCE 254 AA; 27376 MW; C924428643441AD CRC64;

Query Match 22.7%; Score 337; DB 13; Length 254;
Best Local Similarity 31.8%; Pred. No. 5.2e-23;
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Matches 92; Conservative 54; Mismatches 83; Indels 60; Gaps 15;
2Y 6 SLLRNQFILLVLLQIQSLGIDISRPAV-----CATHTIS--PGPKGDD---G 53
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2 TLLOFFSALLLCLSLMATSLLTDD-KPEEKMYSCPIIQCSPAVNGLPGRDGRDGPKG 59
2Y 54 EKGDPGE--EGKHGKVGKMGPKGKIGELGMDGRNGIKTGPIGKKGDKGKGLL---- 106
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2b 60 EKGDPGELGRLQGLPKAGPQGLKGEV-----GQGEKGQKGERGIIVTDDL 107
2Y 107 --GIPGKAGV--CDCGRYKRVFGQGLDISIARLKTSMKFKVNVNVIAGIRETEKFFYIV 163
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2b 108 HROITDLEAKIRVLEDLDSYKXAL-----SLKDVNV-----GKMFVST 148
2Y 164 QEEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFRVFVGVNDLREGQYMET 223
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2b 149 GKKNFKGSLKAGSVLASRNEANTALKDLDPSS--QAYIGSDAQTEGRFMIL 206
2Y 224 DNTPLQYNNNEGPDSPYGHEDCVEMLSGGRWNTDEC-HLTMYFVCE 271
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2b 207 SGGLP-TYSNWKQCEPNN-HKNEDCAVIEDSGKWNLDSCNSNIFIICE 253
2Y 386YK9 PRELIMINARY; PRT; 375 AA.
AC Q86YK9;
2T 01-JUN-2003 (TrEMBLrel. 24, Created)
2T 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
2T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
2E Sufptant, pulmonary-associated protein D.
3N SufptD.
2S Homo sapiens (Human).
2C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
2C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
2X NCBI_TaxID=9606;
2R SEQUENCE FROM N.A.
2P Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
2A Ahearn M.O., Kuldansk S.A., Rajkumar N., Toth E.J., Yi Q.,
2A Nickerson D.A.;
2R Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
2R EMBL; AY216721; AA022991.1; -.
2R GO; GO:0005529; F:sugar binding; IEA.
2R InterPro; IPR001304; Collagen.
2R InterPro; IPR001304; LECTIN_C.
2R Pfam; PF01391; Collagen; 3.
2R Pfam; PF00059; lectin_c; 1.
2R SMART; SM00034; CLECT; 1.
2R PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
2R PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
2R SEQUENCE 375 AA; 37498 MW; 79380764F2B86E67 CRC64;
Query Match 22.7%; Score 337; DB 4; Length 375;
Best Local Similarity 35.2%; Pred. No. 8.5e-23;
Matches 86; Conservative 30; Mismatches 108; Indels 20; Gaps 7;
2Y 46 PGPKEAGPKEVGPAGPQGGAGARGLAGPKGERGVFCRGVGNAGAGSAGAMPQGS 194
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2Y 103 -----KGLLGPKEGKAGT--VDCGRYKRVFGQLDISIARLKTSMKFKVNV--I 149
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2b 195 PGARGPPGLKDGKIPGPKGAKGESGLFDVASLRQVEALQGVQVHLQAFAFSQYKKVELF 254
2Y 150 AGIRETEKFFYIVQEEKNYRESLTHCRIRGMLAMPKDEAANTLIAD-YVAKSGFRVF 208
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2b 255 PNGQSVGSEKIFKTAGVFPFTEAQLLCTQAGQQLASPSRAENALQQLVVAKNE--AAP 312
2Y 209 IGVNDLREGQYMETDNTPLQYNNNEGPDSPYGHEDCVEMLSGGRWNTDEC-HLTMYF 268
2b :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
2b 313 LSWTDSKTEGKFTYPTGSLV-YSNWAPGEENDGSGEDCVEIFPTNGKWNDRACGKRLV 371
```

```
QY 269 VCEF 272
Db 372 VCEF 375
RESULT 12
Q91908 PRELIMINARY; PRT; 251 AA.
ID Q91908
AC Q91908;
2T 01-OCT-2000 (TrEMBLrel. 15, Created)
2T 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
2T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
2E Mannose binding-like lectin precursor.
2R MBL.
2R Brachydanio rerio (Zebrafish) (Danio rerio).
2C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
2C Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
2C Cyprinidae; Danio.
2X NCBI_TaxID=7955;
2R SEQUENCE FROM N.A.
2R MEDLINE=20456722; PubMed=11003389;
2R Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjoldt K.;
2R "the homologue of mannose-binding lectin in the carp family Cyprinidae
2R is expressed at high level in spleen, and the deduced primary
2R structure predicts affinity for galactose.";
2R Immunogenetics 51:955-964(2000).
2R EMBL; AF227738; AAF63469.1; -.
2R HSP; P19999; IAFB.
2R ZFIN; ZDB-GENE-000427-2; mbl.
2R GO; GO:0005529; F:sugar binding; IEA.
2R GO; GO:0007157; P:heterophilic cell adhesion; IEA.
2R InterPro; IPR008161; Clg_helix.
2R InterPro; IPR008160; Collagen.
2R InterPro; IPR001304; LECTIN_C.
2R Pfam; PF01391; Collagen; 2.
2R Pfam; PF00059; lectin_c; 1.
2R ProDom; PD000007; Clg_helix; 1.
2R SMART; SM00034; CLECT; 1.
2R PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
2R PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
2R Collagen; LECTIN; SIGNAL.
2R SIGNAL 1 23 POTENTIAL.
2T CHAIN 24 251 MANNOSE BINDING-LIKE LECTIN.
2T VARIANT 21 21 M -> L.
2T VARIANT 204 204 K -> N.
2R SEQUENCE 251 AA; 26829 MW; 12D0ABD06B6E3B11 CRC64;
Query Match 22.5%; Score 334.5; DB 13; Length 251;
Best Local Similarity 30.4%; Pred. No. 8.7e-23;
Matches 79; Conservative 49; Mismatches 107; Indels 25; Gaps 8;
QY 14 LLLVFLQLQISGLDIDSRPTAEVCATHTISPGPKGDDGEGKDGEGKKGKVGKMGPK 73
Db 11 LLLQLVQLMAGAAB-----PQSLNCFAYA---GVPGTGHNLGPFGRDGRVGRDANGPK 63
QY 74 GIKGELGMDGRNGIKTGPIGKKGKDGKGLGIPGKAGTVCDCGRYKRVFGQLDI 133
Db 64 GEKGEPP-VNVQPPGKAGPPGAGAKGERGSLPGQ-----DC-----MSDSLKS 109
QY 134 SIARLKTSMKFKVNV--AGIRETEKFFYIVQEEKNYRESLTHCRIRGMLAMPKDEAA 191
Db 110 ELQKLSKIALIEKVVNVNFKTFKVGQKYVTVDDVEETFDKGMQYCSSNGGALLVRLTLEE 169
QY 192 NTLIADYVAKSGFRVFVGVNDLREGQYMETDNTPLQYNNNEGPDSPYGHEDCVEM 251
Db 170 NALLKVFVS-SAPKFLFIRITDREKGEFVDTRKLL-TFTNWGNQPNQYKGAQDCGAI 227
QY 252 LSSGRWNTDEC-HLTMYFVCE 271
Db 228 ADSGLMDDVSCDSLYPIICE 247
```

```
RESULT 13
#OTCD8      PRELIMINARY;      PRT;      375 AA.
C Q8TCB8;
T 01-JUN-2002 (T-EMBLrel. 21, Created)
T 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
T 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
E Hypothetical protein.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE FROM N.A.
C TISSUE=Lung;
A Strausberg R.;
L Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
R EMBL; BC02318; AAB94071.1; -.
R GO; GO:0005529; F:sugar binding; IEA.
R InterPro; IPR008161; Clg_helix.
R InterPro; IPR008160; Collagen.
R InterPro; IPR001304; Lectin_C.
R Pfam; PF01391; Collagen; 1.
R Pfam; PF00059; Lectin_C; 1.
R Pfam; PF00059; Lectin_C; 1.
R SMART; SM00034; CLECT; 1.
R PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
R PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
R Collagen; Lactin.
K NON TER 238
FT SEQUENCE 238 AA; 25645 MW; 55C9B5197AAB64E3 CRC64;
SQ
Query Match 22.1%; Score 327.5; DB 13; Length 238;
Best Local Similarity 32.1%; Pred. No. 3.6e-22;
Matches 80; Conservative 48; Mismatches 70; Indels 51; Gaps 12;
QY 39 CATHRTIS--PGKGGD---GKGGDGE--EGKGVGRMGPGKIGKGLGMDGDRNGTGT 91
Db 24 CSAPAVNGLPGRDGRDGPGEGLRGLQGLPGKAGPQGLKGEV----- 71
QY 92 GPIGKGGKGEKGLL-----GIPGEKAGTV--CDGGRYKRVFGQGLDISIARLKTSMK 143
Db 72 GPQGGKGGKGEKGLL-----GIPGEKAGTV--CDGGRYKRVFGQGLDISIARLKTSMK 143
QY 144 FVKNVIAGIRETEEFYIVQEKYRSLTHCRIRGGMLAMPKDEAANTLIADYVAKSG 203
Db 120 DVVNI-----GKMFVSTGKYNFEKGLKCAKAGSVLASPRNEAENTALKDLDPSS 172
QY 204 FRVSTGVNLEREQYMTDNTPLQYNSWNEGPSPDYCHEDCVEMLSGGRWNTDEC- 262
Db 173 --QAVIGLSDAQTEGRFMYLGGPL--TYSNWKPEPNN--HKNECDCAVIEDSGKWNLDGCS 228
QY 263 HLTMYFVCE 271
Db 229 NSNIFICE 237
RESULT 15
Q919Q9      PRELIMINARY;      PRT;      256 AA.
AC Q919Q9;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mannose binding-like lectin precursor.
GN MBL.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20456722; PubMed=11003389;
RA Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjold K.;
RT "The homologue of mannose-binding lectin in the carp family Cyprinidae
RT is expressed at high level in spleen, and the deduced primary
RT structure predicts affinity for galactose.";
RL Immunogenetics 51:955-964(2000).
DR EMBL; AF227737; AAF63468.1; -.
DR HSSP; P35247; 1B08.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lactin_C.
```

DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 256 MANNOSE BINDING-LIKE LECTIN.
FT VARIANT 235 235 S -> T.
SQ SEQUENCE 256 AA; 26934 MW; D019291D1167730D CRC64;

Query Match 21.3%; Score 316; DB 13; Length 256;
Best Local Similarity 31.6%; Pred No. 4.6e-21;
Matches 84; Conservative 39; Mismatches 119; Indels 24; Gaps 8;

2Y 14 ILLVFLQLQISGLDIDSRPTAEVCATHTISPPKGDGEGKDPGEKGKGVGRMGPK 73
Db :||: |||:
11 LLLQLFALQL---LD-GAEPNLNCPAY---GGVPGTGHNLPGRDGRDGDGGAIGPK 62
2Y 74 GIKGELGDMGRGNIGKTPIGKKGDKGKGLLGIPEKKGKAGTVCDGGRKRVQQLDI 133
Db :||: |||:
63 GEKGESG-VSVQPPGKAGPPGAGEKGERGPTGSGSPGS-----ESVLESLS 111
QY 134 STARKTSMKFKVQNV--IAGIRETEEKFYIVQEEKNYRESLTHCRINGMLAMPKDEAA 191
Db :||: |||:
112 EIQLKAKIATFEKVASVGHFRVQGVYITDGVVGTFDQGLKFCXDFGTMVFPRTSAE 171
QY 192 NTLIADYVAKSGFF--RVFIGVNDLEREGQYMTDNTPLQYNSNNWNEGSPSDPYGHEDCV 249
Db :||: |||:
172 NQALLKLVVSSGLSKKPYIGVTDRETEGRFVNTGKQL-TFTNWGFGQPDYKGLQDCG 230
QY 250 EMLSSGRWNTDECHLTMYVCFEIKK 275
Db :||: |||:
231 VIEDSGLWDDGSCGDIRPINCIDNK 256

Search completed: February 24, 2004, 02:24:23
Job time : 67 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: February 24, 2004, 00:35:31; Search time 69 Seconds
(without alignments)
1134.285 Million cell updates/sec

title: US-09-600-932-2
effect score: 1484
equene: 1 MNGFASLLRRNQFILLVLF.....NDTECHLTMYFVCFIKKK 277

coring table: BLOSUM62

Gapop 10.0, Gapext 0.5

earched: 1586107 seqs, 282547505 residues

otal number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase: A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003Bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1484	100.0	277	2	Aay25518 Human col
2	1472	99.2	277	2	Aay41698 Human PRO
3	1472	99.2	277	3	Aab44254 Human PRO
4	1472	99.2	277	4	Aau29073 Human PRO
5	1472	99.2	277	6	Abu58449 Human PRO
6	1472	99.2	277	6	Abu87997 Novel hum
7	1472	99.2	277	6	Abu84312 Human sec
8	1472	99.2	277	6	Abu66186 Human sec
9	1472	99.2	277	6	Abu55576 Human sec
10	1472	99.2	277	6	Abu99516 Human sec
11	1472	99.2	277	6	Abu82755 Human PRO
12	1472	99.2	277	6	Abu89876 Novel hum
13	1472	99.2	277	6	Abu68125 Human sec
14	1472	99.2	277	6	Abu96178 Novel hum
15	1472	99.2	277	6	Abu92609 Human sec
16	1472	99.2	277	6	Abu08686 Human sec
17	1472	99.2	277	6	Abu02738 Human sec
18	1472	99.2	277	6	Abu74892 Human sec
19	1472	99.2	277	6	Abu94654 Human sec
20	1472	99.2	277	6	Abu025200 Novel hum
21	1472	99.2	277	6	Abu85627 Human PRO
22	1472	99.2	277	6	Abu98787 Novel hum
23	1472	99.2	277	6	Abu98002 Novel hum
24	1472	99.2	277	6	Abu91708 Novel hum
25	1472	99.2	277	6	Abu72206 Novel hum

26	1472	99.2	277	6	ABU89401 Human PRO
27	1472	99.2	277	6	ABU86242 Human sec
28	1472	99.2	277	6	ABU67455 Human sec
29	1472	99.2	277	6	ABU80483 Human PRO
30	1472	99.2	277	6	ABR99401 Human sec
31	1472	99.2	277	6	ABR98791 Human sec
32	1472	99.2	277	6	ABO16314 Human sec
33	1472	99.2	277	6	ABR92214 Human sec
34	1472	99.2	277	6	ABO18855 Human sec
35	1472	99.2	277	6	ABR78276 Human sec
36	1472	99.2	277	6	ABU85012 Novel hum
37	1472	99.2	277	6	ABO00151 Novel hum
38	1472	99.2	277	6	ABO11483 Human sec
39	1472	99.2	277	6	ABO02128 Human sec
40	1472	99.2	277	6	ABU88702 Novel hum
41	1472	99.2	277	6	ABU83397 Human sec
42	1472	99.2	277	6	ABO06198 Novel hum
43	1472	99.2	277	6	ABR59234 Human sec
44	1472	99.2	277	6	ABO09296 Human sec
45	1472	99.2	277	6	ABO19160 Novel hum

ALIGNMENTS

RESULT 1
AAY25518
ID AAY25518 standard; protein; 277 AA.
XX
AC AAY25518;
XX
DT 30-SEP-1999 (first entry)
XX
DE Human collectin protein.
XX
KW Collectin; human; antibacterial; antiviral; treatment; infection.
XX
CS Homo sapiens.
XX
PN WO9937767-A1.
XX
PD 29-JUL-1999.
XX
PF 24-JUL-1998; 98WO-JP003328.
XX
PR 23-JAN-1998; 98JP-00011281.
XX
(FUSO) FUSO PHARM IND LTD.
XX
Wakamiya N;
DR WPI; 1999-458691/38.
DR N-PSDB; AAX88323.
XX
New collectin protein of human origin and DNA encoding it.
XX
Claim 1; Page 42-44; 58pp; Japanese.
XX
This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections. This sequence represents the novel human collectin

Query Match 100.0%; Score 1484; DB 2; Length 277;
Best Local Similarity 100.0%; Pred.No. 5e-141;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGKDDGKGPGE 60
DB 1 MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGKDDGKGPGE 60

QY 61 EGKHGKVGMRGPKGKIGELGDMGDRGNTGKTGPIGKGDGKGEKGLGIPGEGKAGTVCD 120
 Db 61 EGKHGKVGMRGPKGKIGELGDMGDRGNTGKTGPIGKGDGKGEKGLGIPGEGKAGTVCD 120
 QY 121 CGRYKFKVQQLDISARLKTSMKFKVKNVIAGIRETEEFYIVQEEKNYRESLTHCRIG 180
 Db 121 CGRYKFKVQQLDISARLKTSMKFKVKNVIAGIRETEEFYIVQEEKNYRESLTHCRIG 180
 QY 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLEREQYMTDNTPLQYNNWNEGEPS 240
 Db 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLEREQYMTDNTPLQYNNWNEGEPS 240
 QY 241 DPYGHEDCVEMLSGRWNTDTECHLTMYVCFEIKKK 277
 Db 241 DPYGHEDCVEMLSGRWNTDTECHLTMYVCFEIKKK 277

RESULT 2
 ID AAY41698 standard; protein; 277 AA.
 AC AAY41698;
 XX 07-DEC-1999 (first entry)
 XX Human PRO702 protein sequence.
 XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX Homo sapiens.
 XX WO9946281-A2.
 XX 16-SEP-1999.
 XX 08-MAR-1999; 99WO-US005028.
 XX 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-0004020.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 23-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079666P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.

PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082589P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082767P.
 PR 23-APR-1998; 98US-0082796P.
 PR 27-APR-1998; 98US-0083336P.
 PR 28-APR-1998; 98US-0083332P.
 PR 29-APR-1998; 98US-0083392P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 29-APR-1998; 98US-0083500P.
 PR 29-APR-1998; 98US-0083545P.
 PR 29-APR-1998; 98US-0083554P.
 PR 29-APR-1998; 98US-0083586P.
 PR 29-APR-1998; 98US-0083599P.
 PR 30-APR-1998; 98US-0083742P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 06-MAY-1998; 98US-0084441P.
 PR 07-MAY-1998; 98US-0084598P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 07-MAY-1998; 98US-0084627P.
 PR 07-MAY-1998; 98US-0084637P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 13-MAY-1998; 98US-0085323P.
 PR 13-MAY-1998; 98US-0085338P.
 PR 13-MAY-1998; 98US-0085339P.
 PR 15-MAY-1998; 98US-0085573P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085689P.
 PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 15-MAY-1998; 98US-0085704P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.

(GETH) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

N-PSDB; AAZ33973.

New secreted and transmembrane polypeptides and their polynucleotides,
 useful for treating blood coagulation disorders, cancers and cellular
 adhesion disorders.

Claim 12; Fig 37; 530pp; English.

The present invention describes secreted and transmembrane polypeptides
 and their polynucleotides. The nucleotide sequences are useful as sources
 of probes, primers, for chromosome mapping, and for generation of
 antisense sequences. They can also be used to create transgenic animals.

The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AA41685 to AA41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention

Sequence 277 AA;

Query Match 99.2%; Score 1472; DB 2; Length 277;
Best Local Similarity 99.3%; Pred. No. 8.1e-140;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MNGFASLLRRNQFILLVFLFLLQISGLDIDSRPTAEVCATHTISPGKGDGKGDGPG 60
1 MNGFASLLRRNQFILLVFLFLLQISGLDIDSRPTAEVCATHTISPGKGDGKGDGPG 60

61 EGKHGKVGMRGPKIGKELGDMGDEGNIGTKPTGKKGDKGKGLLIPGKKGAGTVCD 120
61 EGKHGKVGMRGPKIGKELGDMGDEGNIGTKPTGKKGDKGKGLLIPGKKGAGTVCD 120

121 CGRYKFKVGQDLSIARLKTSMKFKVNIAGIRETEKFFYIVQEEKNYRESLTHCRIRG 180
121 CGRYKFKVGQDLSIARLKTSMKFKVNIAGIRETEKFFYIVQEEKNYRESLTHCRIRG 180

181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQYSNWNEGEPS 240
181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQYSNWNEGEPS 240

241 DPYGHEDCVEMLSGRWNTDECHLTMYFVCFEIKKK 277
241 DPYGHEDCVEMLSGRWNTDECHLTMYFVCFEIKKK 277

RESULT 3
AB44254
AAB44254 standard; protein; 277 AA.
AAB44254;

08-FEB-2001 (first entry)
Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.
Human; secreted protein; transmembrane protein; PRO; EST; cytotstatic;
expressed sequence tag; detection; cancer.
Homo sapiens.
WO200053756-A2.
14-SEP-2000.
18-FEB-2000; 2000WO-US004341.
08-MAR-1999; 99WO-US005028.
12-MAR-1999; 99US-0123957P.
29-MAR-1999; 99US-0126773P.
21-APR-1999; 99US-0130232P.
28-APR-1999; 99US-0131445P.
14-MAY-1999; 99US-0134287P.
23-JUN-1999; 99US-0141037P.
26-JUL-1999; 99US-0145698P.
29-OCT-1999; 99US-0162506P.
30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
16-DEC-1999; 99WO-US030095.
30-DEC-1999; 99WO-US031243.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.

XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
DR WPI, 2000-611443/58.
DR N-PSDB; AAC78480.
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX Claim 12; Fig 37; 636pp; English.
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytotstatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX Sequence 277 AA;

Query Match 99.2%; Score 1472; DB 3; Length 277;
Best Local Similarity 99.3%; Pred. No. 8.1e-140;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MNGFASLLRRNQFILLVFLFLLQISGLDIDSRPTAEVCATHTISPGKGDGKGDGPG 60
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121 CGRYKFKVGQDLSIARLKTSMKFKVNIAGIRETEKFFYIVQEEKNYRESLTHCRIRG 180
121 CGRYKFKVGQDLSIARLKTSMKFKVNIAGIRETEKFFYIVQEEKNYRESLTHCRIRG 180

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181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQYSNWNEGEPS 240

241 DPYGHEDCVEMLSGRWNTDECHLTMYFVCFEIKKK 277
241 DPYGHEDCVEMLSGRWNTDECHLTMYFVCFEIKKK 277

RESULT 4
AAU29073
ID AAU29073 standard; protein; 277 AA.
XX AAU29073;
AC AAU29073;
XX 18-DEC-2001 (first entry)
XX Human PRO polypeptide sequence #50.
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; cervix; liver; genetic disorder.
XX Homo sapiens.

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XX WO200168848-A2.
PN
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
XX 01-MAR-2000; 2000WO-US005601.
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XX 02-MAR-2000; 2000WO-US005841.
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XX 03-MAR-2000; 2000US-0187202P.
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XX 06-MAR-2000; 2000US-0186968P.
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XX 14-MAR-2000; 2000US-0189320P.
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XX 14-MAR-2000; 2000US-0189328P.
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XX 15-MAR-2000; 2000WO-US006884.
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XX 03-MAY-2000; 2000US-0201516P.
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XX 17-MAY-2000; 2000WO-US013705.
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XX 22-MAY-2000; 2000WO-US014042.
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XX 30-MAY-2000; 2000WO-US014941.
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XX 02-JUN-2000; 2000WO-US015264.
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XX 05-JUN-2000; 2000US-0209832P.
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XX 28-JUL-2000; 2000WO-US020710.
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XX 22-AUG-2000; 2000US-00644848.
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XX 24-AUG-2000; 2000WO-US023328.
XX
XX 08-NOV-2000; 2000WO-US030952.
XX
XX 01-DEC-2000; 2000WO-US032678.
XX
XX 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
XX
XX N-PSDB; AAS45974.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumors, such as prostate and breast tumors, in mammals and to
XX screen for modulators of the compounds.
XX
XX Claim 11; Fig 100; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX The PRO polypeptides and their associated nucleic acids can be used to
XX detect the presence of a tumour in a mammal by comparing the level of
XX expression of a PRO polypeptide in a test sample of cells from the animal
XX and a control sample of normal cells, whereby a higher level of
XX expression in the test sample indicates the presence of a tumour in the
XX mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
XX and rabbits but are preferably human. The polypeptides can be used to
XX stimulate tumour necrosis factor (TNF) alpha release from human blood,
XX when contacted with it. A specific polypeptide can be used to stimulate
XX the proliferation or differentiation of chondrocyte cells. The PRO
XX proteins can be used to determine the presence of tumours and also
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CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX SQ Sequence 277 AA;
XX
XX Query Match 99.2%; Score 1472; DB 4; Length 277;
XX Best Local Similarity 99.3%; Pred. No. 8.1e-140;
XX Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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XX QY 1 MNGFASLLRRNQFILLVFLFLLQIOSLGLDIDSRPTAEVCATHTTISPGPKGDDGKGDPE 60
XX Db 1 MNGFASLLRRNQFILLVFLFLLQIOSLGLDIDSRPTAEVCATHTTISPGPKGDDGKGDPE 60
XX QY 61 EGKHGKVGMRGPKIGKELGDMGDGRNIGKTGPIGKKGDKGKGLLGPCEKKGAGTVC 120
XX Db 61 EGKHGKVGMRGPKIGKELGDMGDGRNIGKTGPIGKKGDKGKGLLGPCEKKGAGTVC 120
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XX QY 181 GMLAMPKDEAANTLIADYVAKSGFERVFGVNDLREGOYMTDNTPLQYNNWNEGPS 240
XX Db 181 GMLAMPKDEAANTLIADYVAKSGFERVFGVNDLREGOYMTDNTPLQYNNWNEGPS 240
XX QY 241 DPYGHEDCVEMLSGGRWNTDECHLTWYFVCEFIKXXX 277
XX Db 241 DPYGHEDCVEMLSGGRWNTDECHLTWYFVCEFIKXXX 277
XX
XX RESULT 5
XX ABUS8449
XX ID ABUS8449 standard; protein; 277 AA.
XX AC ABUS8449;
XX
XX DT 15-APR-2003 (first entry)
XX
XX DE Human PRO polypeptide #50.
XX
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;
XX antibody-dependent enzyme mediated prodrug therapy.
XX
XX OS Homo sapiens.
XX
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX
XX PF 21-JUN-2002; 2002US-00176492.
XX
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 21-OCT-1997; 97US-0063486P.
XX PR 24-OCT-1997; 97US-0063120P.
XX PR 24-OCT-1997; 97US-0063121P.
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XX PR 13-NOV-1997; 97US-0065311P.
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XX PR 24-NOV-1997; 97US-0066466P.
XX PR 24-NOV-1997; 97US-0066772P.
XX PR 11-DEC-1997; 97US-0069335P.
XX PR 12-DEC-1997; 97US-0069425P.
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Best Local Similarity 99.3%; Pred. No. 8.le-140;

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Qy	121	CGRYRKFGVQLDISIARLKTSMKFKVKNVIAGIRETEKFFYIVQEEKNYRESLTHCRIRG	180
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Qy	181	GMLAMPKDEAANTLIADYVAKSGFRRVFIGVNDLEREGVMTDNTPLQNSWNNEGEPS	240
Db	181	GMLAMPKDEAANTLIADYVAKSGFRRVFIGVNDLEREGVMTDNTPLQNSWNNEGEPS	240
Qy	241	DPYGHEDCVEMLSGSRWNTDTECHLTMYFVCFEIKKKK	277
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RESULT 7

ABU84312

ID ABU84312 standard; protein; 277 AA.

XX AC ABU84312;

XX DT 02-AUG-2003 (first entry)

XX DE Human secreted/transmembrane protein (PRO) #50.

XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;

XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

XX OS Homo sapiens.

XX PN US2003032112-A1.

XX PD 13-FEB-2003.

XX PF 21-JUN-2002; 2002US-00176756.

XX PR 18-SEP-1997; 97US-0059263P.

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XX PN US2003032113-A1.
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QY 121 CORYKRFVQQLDISIARLKTSMKFVKVNIAGIRTEEEKFYIVQEEKYRESLTHCRIRG 180
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QY 181 GMLAMPKDEAAANTLIADYVAKSGFRFVIGVNDLERSQYMFDTNPLQNSYNNWGEPS 240
DB 181 GMLAMPKDEAAANTLIADYVAKSGFRFVIGVNDLERSQYMFDTNPLQNSYNNWGEPS 240
QY 241 DPYGHEDCVELSSGRWNTTECHLTMYFVCFEIKKKK 277
DB 241 DPYGHEDCVELSSGRWNTTECHLTMYFVCFEIKKKK 277

RESULT 12
ABU89876
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AC ABU89876;
XX
DT 11-AUG-2003 (first entry)
XX
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KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX affinity purification.
XX
OS Homo sapiens.
XX
PN US2003036147-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187741.
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b 121 CGYRKFVGGQDLSIARLKTSMKFKVQVNIAGIRETEEFYIVQEKYRSLTHCRIRG 180

Y 181 GMLAMPKDEAANTLIADYVAKSGFPRVFIGNDLRREGQYMTDNTPLQNYNNWGEPS 240
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Y 241 DPYGHEDCVEMLSGGRWNTDTECHLTMYFVCEFIKXXX 277
b 241 DPYGHEDCVEMLSGGRWNTDTECHLTMYFVCEFIKXXX 277

RESULT 13
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X 11-AUG-2003 (first entry)
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X extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
X chondrocyte; proliferation; differentiation; cartilage disorder;
X bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
X adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
X liver; drug screening; transgenic animal; genetic analysis;
X antiarthritic; vulnervary; gene therapy.
X
X Homo sapiens.
X
X US2003027264-A1.
X
X 06-FEB-2003.
X
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DB	121	CGRYKFKVQGLDISARLKTSMKFKYVNIAGIRETEEFYIYVOEKNYRESLTHCKIRG 180	PR	15-APR-1998;	98US-0081838P.
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Query Match 99.2%; Score 1472; DB 6; Length 277;
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DB 61 EKGKGVGRMGPKIGKELGDMGDRGNIGKTGPIGKKGKGLLGIPEGKKGAGTVCD 120
QY 121 CGRYKFGQLDISARLKTSMKFVKVNIAGIRTEEFKYYIIOEKNYRESLTHCIRG 180
DB 121 CGRYKFGQLDISARLKTSMKFVKVNIAGIRTEEFKYYIIOEKNYRESLTHCIRG 180
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DB 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLEREGQYMTDNTPLQYNSWNEGEPS 240
QY 241 DPYGHEDCVEMLSGRWNTDTECHLTMYFVCFIKKKK 277
DB 241 DPYGHEDCVEMLSGRWNTDTECHLTMYFVCFIKKKK 277

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Job time : 72 secs

GenCore version 5.1.6
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4 protein - protein search, using sw model

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(without alignments)
801.302 Million cell updates/sec

title: US-09-600-932-2

effect score: 1484

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coring table: BLOSUM62

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searched: 141681 seqs, 52070155 residues

total number of hits satisfying chosen parameters: 141681

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	349.5	23.6	369	1	PSPD_BOVIN	P35246 bos taurus
3	340	22.9	374	1	PSPD_MOUSE	P50404 mus musculus
4	337	22.7	375	1	PSPD_HUMAN	P35247 homo sapien
5	333	22.4	374	1	PSPD_RAT	P35248 rattus norv
6	330.5	22.3	371	1	CL46_BOVIN	Q8mhz9 bos taurus
7	328.5	22.1	371	1	CONG_BOVIN	P33805 bos taurus
8	305.5	20.5	247	1	PSPA_RABIT	P12842 coryctolagus
9	290	19.5	238	1	MABA_RAT	P19999 rattus norv
10	290	19.5	244	1	MABC_MOUSE	P41317 mus musculus
11	289.5	19.5	248	1	MABC_HUMAN	P11226 homo sapien
12	285.5	19.2	249	1	PSPA_PIG	P49874 sus scrofa
13	284.5	19.2	249	1	MABC_BOVIN	O02659 bos taurus
14	284	19.1	248	1	PSPA_HUMAN	P07714 homo sapien
15	280	18.9	248	1	PSPA_CANFA	P06908 canis famil
16	279	18.8	244	1	MABC_RAT	P08661 rattus norv
17	277	18.7	248	1	PSPA_RAT	P38427 rattus norv
18	270.5	18.2	239	1	MABA_MOUSE	P39039 mus musculus
19	270	18.2	247	1	PSPA_CAVPO	P50403 cavia porce
20	269.5	18.2	248	1	PSPA_MOUSE	P35242 mus musculus
21	207	13.9	689	1	CAS2_HUMAN	Q4055 homo sapien
22	203	13.7	688	1	CAS3_MOUSE	Q07643 mus musculus
23	196.5	13.2	289	1	Q077_HUMAN	Q07642 homo sapien
24	196	13.2	1775	1	CA14_DROME	P08120 drosophila
25	192.5	13.0	2944	1	CA17_HUMAN	Q02388 homo sapien
26	191.5	12.9	1366	1	CA21_HUMAN	P08123 homo sapien
27	191	12.9	1022	1	CA26_CHICK	P15988 gallus gall
28	187.5	12.6	508	1	OT01_ONCKE	P33371 oncorhynch
29	187.5	12.6	518	1	MTCO_MOUSE	Q60754 mus musculus
30	187	12.6	1029	1	CA26_MOUSE	Q02788 mus musculus
31	186	12.5	1025	1	CA16_MOUSE	Q04857 mus musculus
32	186	12.5	1736	1	CA2B_MOUSE	Q64739 mus musculus
33	185.5	12.5	674	1	CA1A_CHICK	P08125 gallus gall

RESULT 1

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DT	01-NOV-1995 (Rel. 32, Created)					P20908 homo sapien
DT	28-FEB-2003 (Rel. 41, Last sequence update)					P12105 gallus gall
DT	10-OCT-2003 (Rel. 42, Last annotation update)					P20785 gallus gall
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GN	CL43.					O46392 canis famil
OS	Bos taurus (Bovine).					P05997 homo sapien
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					P12109 homo sapien
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RX	MEDLINE=22414671; PubMed=12527419;					
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RA	Holmskov U.;					
RT	"Genomic and molecular characterization of CL-43 and its proximal					
RT	promoter."					
RL	Biochim. Biophys. Acta 1625:1-10(2003).					
RN	[2]					
RP	SEQUENCE OF 21-321 FROM N.A., AND PARTIAL SEQUENCE.					
RC	TISSUE=Liver;					
RX	MEDLINE=94216283; PubMed=8163480;					
RA	Lim B.-L., Willis A.C., Reid K.B.M., Lu J., Laursen S.B.,					
RA	Jensenius J.C., Holmskov U.;					
RT	"Primary structure of bovine collectin-43 (CL-43). Comparison with					
RT	conglutinin and lung surfactant protein-D."					
RL	J. Biol. Chem. 269:11820-11824(1994).					
CC	!- FUNCTION: Lectin that binds to various sugars: mannose = manNAc >					
CC	fucose > galNAc > glucose = maltose > galactose > lactose >					
CC	!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.					
CC	!- SUBCELLULAR LOCATION: Secreted.					
CC	!- TISSUE SPECIFICITY: Liver specific.					
CC	!- PTM: Hydroxylated (potential).					
CC	!- SIMILARITY: Contains 1 collagenous domain.					
CC	!- SIMILARITY: Contains 1 C-type lectin family domain.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC	the European Bioinformatics Institute. There are no restrictions on its					
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CC	HSSP; P35247; 1B08.					
CC	InterPro; IPR008160; Collagen.					
CC	InterPro; IPR001304; Lectin_C.					

C P50404;
T 01-OCT-1996 (Rel. 34, Created)
T 01-OCT-1996 (Rel. 34, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
S SFTPD OR SFTPD.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=C57BL/6 X CBA; TISSUE=Lung;
C MEDLINE=96094460; PubMed=7499852;
X Matwani M., White R.A., Gao N., Dowler L.L., Tauber A.I., Sastry K.N.;
A "Mus surfactant protein-D. cDNA cloning, characterization, and gene
T localization to chromosome 14."
T L J. Immunol. 155:5671-5677(1995).
N [2]
P SEQUENCE FROM N.A.
C STRAIN=129/SV;
X MEDLINE=99244602; PubMed=10226065;
A Lawson P.R., Perkins V.C., Holmskov U., Reid K.B.;
T "Genomic organization of the mouse gene for lung surfactant protein
T D.";
T Am. J. Respir. Cell Mol. Biol. 20:953-963(1999).
N [3]
P SEQUENCE FROM N.A.
A Fisher J.H., Sheftelyevich V.V.;
T "Surfactant protein-D regulates surfactant phospholipid homeostasis in
T vivo."
T Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
N [4]
P SEQUENCE FROM N.A.
X MEDLINE=22388257; PubMed=12477932;
A Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;
A Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
A Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
A Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences."
T Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
L C -1- FUNCTION: Contributes to the lung's defense against inhaled
C microorganisms. Binds strongly maltose residues and to a lesser
C extent other alpha-glucosyl moieties. It could participate in the
C extracellular reorganization or turnover of pulmonary surfactant.
C -1- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
C -1- SUBCELLULAR LOCATION: Extracellular.
C -1- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
C protein. There are 4 surfactant-associated protein: 2 collagenous,
C carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small
C hydrophobic proteins (SP-B and SP-C).
C -1- SIMILARITY: Contains 1 collagenous domain.
C -1- SIMILARITY: Contains 1 C-type lectin family domain.
C
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CC or send an email to license@iesb-sib.ch).
CC -----
DR EMBL; L40156; AAA92021.1; .
DR EMBL; AF047742; AAD31380.1; .
DR EMBL; AF047741; AAD31380.1; JOINED.
DR EMBL; AF192134; AAF15277.1; .
DR EMBL; BC003705; AAH03705.1; .
DR HSSP; P35247; IBO8.
DR MGI; MGI:105515; Sftpd.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF01391; Collagen; 3.
DR Pfam; PF00059; Lectin C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS00411; C-TYPE LECTIN_2; 1.
DR KW Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
KW Signal; Lectin; Collagen; Repeat; Coiled coil.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 374 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
FT D.
FT DOMAIN 45 221 COLLAGEN-LIKE.
FT DOMAIN 222 253 COILED COIL (POTENTIAL).
FT DOMAIN 278 374 C-TYPE LECTIN (SHORT FORM).
FT DISULFID 280 372 BY SIMILARITY.
FT DISULFID 350 364 BY SIMILARITY.
FT CARBOHYD 89 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 374 AA; 37688 MW; F5034261263F43E4 CRC64;

Query Match 22.9%; Score 340; DB 1; Length 374;
Best Local Similarity 32.4%; Pred. No. 1.3e-21;
Matches 80; Conservative 34; Mismatches 107; Indels 26; Gaps 6;

QY 46 PGPKGDDGEGD---PGEEGHGKVGVRGPKGIGKGLGDMGDRGNCKTGPIGKKGDKGE 102
DB 134 PGPKEGPKGEVGPAGPVGQSTGAKSTGPKGERGAPGVQCAPNAGAAAGPAGPQGA 193
QY 103 KGLLGIPGEKGAGVDCGGRYKRVFGOLDI-SIARLKTGKFKVNIAGI----- 152
DB 194 PGRGPPGLKGRGVPGD---RGIKGESGLPDSALRQQMEALKGLQRLVAFSHYQK 249
QY 153 -----RETTEKFIYVQEEKNYRESLTHCRIGGMAMPKDEAANTLIADYVAKSGFF 205
DB 250 AALFPDGRSVGDKIPRTADSEKPFDAQEMCKQAGQJASPRSTATENAAIQOLITAN-K 308
QY 206 RVFIVGNLDERGQYMTDTPLQNSYNNWNEGEPSPYGHEDCYEMLSSGRWNTDECHLT 265
DB 309 AAFLSMTDVGTEGKFTYTGPELV-YSNWPAGEPNNNGAENCVEIFTNGQWNDKACGEQ 367
QY 266 MYFVCEP 272 .
DB 368 RLVICEF 374

RESULT 4
PSPD_HUMAN
ID PSPD_HUMAN STANDARD; PRT; 375 AA.
AC F35247;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
GN SFTPD OR SFTPD OR PSPD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93155122; PubMed=8428971;
RA Crouch E., Rust K., Veille R., Donis-Keller H., Grosso L.;

RT "Genomic organization of human surfactant protein D (SP-D). SP-D is
RL encoded on chromosome 10q22.2-23.1.";
RN J. Biol. Chem. 268:2976-2983(1993).
RP [2]
RC SEQUENCE FROM N.A., AND SEQUENCE OF 214-243.
RX TISSUE-Amniotic fluid, and Lung;
RY MEDLINE=92322003; PubMed=1339284;
RA Lu J., Willis A.C., Reid K.B.M.;
RT "Purification, characterization and cDNA cloning of human lung
RL surfactant protein D.";
RN Biochem. J. 284:795-802(1992).
RP [3]
RC SEQUENCE OF 60-375 FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Lung;
RY MEDLINE=91378578; PubMed=1398081;
RA Rust K., Grosso L., Zhang V., Chang D., Persson A., Longmore W.,
RC Cai G.-Z., Crouch E.;
RT "Human surfactant protein D: SP-D contains a C-type lectin
RL carbohydrate recognition domain.";
RN Arch. Biochem. Biophys. 290:116-126(1991).
RP [4]
RC X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=99197291; PubMed=10368295;
RA Hakansson K., Lim N.K., Hoppe H.-J., Reid K.B.M.;
RT "Crystal structure of the trimeric alpha-helical coiled-coil and the
RL three lectin domains of human lung surfactant protein D.";
RN Structure 7:255-264(1999).
RP [5]
RC -I- FUNCTION: Contributes to the lung's defense against inhaled
RX microorganisms. Binds strongly to maltose residues and to a lesser
RY extent other alpha-glucosyl moieties. It could participate in the
RA extracellular reorganization or turnover of pulmonary surfactant.
RT -I- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
RL -I- SUBCELLULAR LOCATION: Extracellular.
RN -I- PTM: The N-terminus is blocked.
RP -I- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
RX protein. There are 4 surfactant-associated proteins: 2 collagenous,
RY carbohydrate-binding glycoproteins (SP-A and SP-B) and 2 small
RA hydrophobic proteins (SP-C and SP-D).
RT -I- SIMILARITY: Contains 1 collagenous domain.
RL -I- SIMILARITY: Contains 1 C-type lectin family domain.
RN
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RP
RX EMBL; L05485; AAB59450.1;
RY EMBL; L05483; AAB59450.1; JOINED.
RA EMBL; L05484; AAB59450.1; JOINED.
RT EMBL; X65018; CAA46152.1;
RN PIR; A45225; A45225.
RP PDB; 1B08; 29-NOV-99.
RX PDB; 1M7L; 27-NOV-02.
RY Genew; HGNC:10803; SFTPD.
RA MIM; 178635;
RT GO; GO:0005530; F.lectin, TAS.
RN InterPro; IPR008161; Clg_helix.
RX InterPro; IPR008160; Collagen.
RY InterPro; IPR001304; Lectin_C.
RA Pfam; PF01391; Collagen; 4.
RT Pfam; PF00059; lectin c; 1.
RN ProDom; PD000007; Clg_helix; 1.
RX SMART; SM00034; CLECT; 1.
RY PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
RA PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
RT Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
RL Signal; Lectin; Collagen; Repeat; Coiled coil; 3D-structure.
RN SIGNAL 1 20 BY SIMILARITY.
RP CHAIN 21 375 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
RX D.

FT DOMAIN 46 222 COLLAGEN-LIKE.
FT DOMAIN 223 252 COILED COIL (POTENTIAL).
FT DOMAIN 279 375 C-TYPE LECTIN (SHORT FORM).
FT DISULFID 281 373
FT DISULFID 351 365
FT CARBOHYD 90
FT MOD RES 78 78 N-LINKED (GLCNAC... (POTENTIAL).
FT MOD RES 87 87 HYDROXYLATION (BY SIMILARITY).
FT MOD RES 96 96 HYDROXYLATION (BY SIMILARITY).
FT MOD RES 99 99 HYDROXYLATION (BY SIMILARITY).
FT MOD RES 171 171 HYDROXYLATION (BY SIMILARITY).
FT MOD RES 177 177 HYDROXYLATION (BY SIMILARITY).
FT CONFLICT 31 31 M -> T (IN REF. 2).
FT CONFLICT 59 59 P -> F (IN REF. 3).
FT CONFLICT 122 122 A -> P (IN REF. 2).
FT CONFLICT 180 180 T -> A (IN REF. 2).
FT CONFLICT 206 206 D -> P (IN REF. 3).
FT CONFLICT 374 374 E -> EH (IN REF. 3).
FT HELIX 227 253
FT TURN 254 256
FT STRAND 267 260
FT TURN 261 262
FT STRAND 263 272
FT HELIX 274 283
FT TURN 284 285
FT STRAND 287 288
FT HELIX 294 307
FT TURN 308 308
FT STRAND 311 316
FT TURN 321 322
FT STRAND 325 325
FT TURN 327 328
FT STRAND 331 331
FT TURN 337 337
FT TURN 339 340
FT HELIX 345 347
FT STRAND 351 354
FT TURN 356 357
FT STRAND 360 363
FT TURN 365 366
FT STRAND 369 375
SQ SEQUENCE 375 AA; 37702 MW; 2986B2699FC01A6A CRC64;

Query Match 22.7%; Score 337; DB 1; Length 375;
Best Local Similarity 35.2%; Pred. No. 2.3e-21;
Matches 86; Conservative 28; Mismatches 110; Indels 20; Gaps 6;

QY 46 PGPKGDDGKGPGEKGKGVGRMGPKGIKGLGMDGRGNIGTKGPICK----- 95
Db 135 PGPKEAGPKGVGAPGVGSGAGAGLAGPKGGERGVGPGNTGAGSAGAMGPQS 194
QY 97 ---KGDKEKGLLGIPEKKGAGT--VDCGRYRKFGVQLDLSIARLKTSMKFKVAV--I 149
Db 195 FGARGPPGLKGDGKIPGDGKAGGESGLPDVASLRQQVEALQGVQHLQAAFSQYKKVELF 254
QY 150 AGIRTEEEKFYIVQEEKKNVRESLTHCRIRGGMLAMPKDEAANTLIAD-YVAKSGFFRVF 208
Db 255 PNGQSVGEKIKETAGFYKFTTEAQLCTQAGGQLASPSAENAAQLQVLVAKNE--AAF 312
QY 209 IGVDLREGEQYMTDNTPLQYNNWNEGSPSPYGHEDCVEMLSGSRWNTDTECHITWTF 268
Db 313 LSWTDSKTEGKFTYPTGESLV-YSNWAPGEPNDGSDCEVFTNGKWNDRACGKRLV 371
QY 269 VCEF 272
Db 372 VCEF 375

RESULT 5
PSPD_RAT
ID PSPD_RAT STANDARD; PRT; 374 AA.
AC P35246;
DT 01-FEB-1994 (Rel. 28, Created)

FT	MOD_RES	176	176		HYDROXYLATION.
FT	CONFLICT	89	89	N -> E (IN REF. 2).	
FT	CONFLICT	164	164	K -> C (IN REF. 2).	
SQ	SEQUENCE	374 AA;	37561 MW;	DB2BB5E399DBA43C CRC64;	
	Query Match	22.4%;	Score 333;	DB 1;	Length 374;
	Best Local Similarity	32.1%;	Pred.No.5.le-21;		
	Matches	78;	Conservative	36;	Mismatches 111;
					Indels 18;
					Gaps 5;
QY	46	PPKGGDDDEKGD---	PGEEGKHGKVGRMGPKGIKGELGMDGRGNIGTKTPIGKKDKGE	102	
Db	134	PPKGEAGPKEVGAPCMQGSAGAKGPACGKBERGAPGEGGAPGNAGAAGPAGPAGPOGA	193		
QY	103	KLLGLIPGEKKAAGTVCDCG-----	VYRKFVGGQIDISIARLKTSMKFVN--VI	149	
Db	194	PSRGPPGLKDRGAPGDRGIKGESGLPDSAAALRQQMEALNGKLORLEAFSRYKKAALF	253		
QY	150	AGIRETEKFFYIVQEIEKNVRESLTHTCRINGGMAMPKDEAAANTLIADYVAKSGFRRVFI	209		
Db	254	PDGSGVDGXIFRAANSSEPEDAKEMCRQGQLASPRSATENAAVQVLTAHS-KAFL	312		
QY	210	GYNDLEREGQMFTNDTPLONYNNWNEGPSDPYGHEDCVEMLSGSRNNDTECHTWTVFV	269		
Db	313	SMTDVGTGCKTYPTGEALY-YSNWAPGEPNNNGAENCVEIFTNGMWDKACGQRLLVI	371		
QY	270	CEF 272			
Db	372	CEF 374			
	RESULT 6				
ID	CL46_BOVIN				
ID	CL46_BOVIN	STANDARD;	PRT;	371 AA.	
AC	Q8MZ9;				
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Collectin-46 precursor (CL-46) (46 kDa collectin).				
CL46					
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
ON	NCBI_TaxID=9913;				
RX	[1]				
RN	SEQUENCE FROM N.A.				
RP	Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M.,				
RA	Skjodet K., Holmskov U.;				
RA	"CL-46", a novel collectin highly expressed in the bovine thymus and				
RT	liver.";				
RL	SUBMITTED (MAY-2002) to the EMBL/GenBank/DDBJ databases.				
CC	-! SUBUNIT: Oligomeric complex of 4 set of homotrimers (By				
CC	similarity).				
CC	-! SUBCELLULAR LOCATION: Secreted.				
CC	-! TISSUE SPECIFICITY: Highly expressed in thymus and liver.				
CC	-! PTM: Hydroxylated (Potential).				
CC	-! SIMILARITY: Contains 1 collagenous domain.				
CC	-! SIMILARITY: Contains 1 C-type lectin family domain.				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; AF509589; AAM34742.1; -				
DR	EMBL; AF509589; AAM34743.1; -				
DR	InterPro; IPR008160; Collagen.				
DR	InterPro; IPR001304; Lectin_C.				
DR	Pfam; PF01391; Collagen; 2.				
DR	Pfam; PF00059; lectin c; 1.				

DR SMART; SMO0034; CLEST; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE; PS00641; C-TYPE LECTIN 2; 1.
 KW Lactin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane;
 KW Collagen; Repeat; Calcium; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 371
 FT DOMAIN 46 216
 FT SITE 201 203
 FT DISULFID 275 369
 FT DISULFID 347 361
 FT CARBOHYD 90 90
 SQ SEQUENCE 371 AA; 37445 NW; 109AC45A91420E83 CRC64;
 Query Match 22.3%; Score 330.5; DB 1; Length 371;
 Best Local Similarity 30.1%; Pred. No. 8.2e-21;
 Matches 84; Conservative 35; Mismatches 105; Indels 55; Gaps 8;
 QY 46 PGPFGDGEKGDG-----GEEGKHKVGRMPKIGKELGMDGRGNI-----GKTGP 93
 DB 96 PGPFGDTPPGPPGPGAGREGPSGKQSGMPGCTPGKDTGPKGGMGAPGQGGSPG 155
 QY 94 IGKKGDKGKGLGTPGKAGT-----V 118
 DB 156 AGLKRGAPGELGAPGSGAGVAGAPAGIOPQPGSGARGPPGLKGDGDPGERGAKGESGL 215
 QY 119 CDCGRYKRVKQGLDISIARLKTSMKFNVI--AGIRETEKFFYIVQEEKVRESLTHC 176
 DB 216 ADVNALKQRTVILEGQLQLQAPSRYSKAVLFPDQAVGKKIKPTAGAVKVSYDAQCLC 275
 QY 177 RIRGGMAMPKDEANTLIADTV-AKSGFFRVFIOVDLREGQVMTDNTPLQYNNWN 235
 DB 276 REAKGQLAFGRSAEAEVAQIVRAKN--DAFLSMNDISTEGKFTYPTGBSLV-YGNA 332
 QY 236 EGPSPYDG--HEDCVEMLSGRWNTDECHLMYVCECF 272
 DB 333 SGEPNNAGQPCNCVQIVREGKNDVFCSEPLLVICEF 371
 RESULT 7
 CONG BOVIN STANDARD; PRT; 371 AA.
 AC P23805; O97748;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Conglutinin precursor.
 GN CGN1.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93213261; PubMed=8460993;
 RA Suzuki Y., Yin Y., Makino M., Kurimura T., Wakamiya N.;
 RT "Cloning and sequencing of a cDNA coding for bovine conglutinin.";
 RL Biochem. Biophys. Res. Commun. 191:335-342(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93277452; PubMed=7684896;
 RA Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;
 RT "The cDNA cloning of conglutinin and identification of liver as a
 primary site of synthesis of conglutinin in members of the Bovidae.";
 RL Biochem. J. 292:157-162(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94215917; PubMed=8163202;
 RA Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
 Tauber A.I., Sastry K.N.;

RT "Bovine conglutinin (BC) mRNA expressed in liver: cloning and
 characterization of the BC cDNA reveals strong homology to surfactant
 protein-D.";
 RL Gene 141:277-281(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Semen;
 RX MEDLINE=94267222; PubMed=8207234;
 RA Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
 Tauber A.I., Sastry K.N.;
 RT "Bovine conglutinin gene exon structure reveals its evolutionary
 relationship to surfactant protein-D.";
 RL J. Immunol. 153:173-180(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94128104; PubMed=8297370;
 RA Kawasaki N., Itoh N., Kawasaki T.;
 RT "Gene organization and 5'-flanking region sequence of conglutinin: a
 C-type mammalian lectin containing a collagen-like domain.";
 RL Biochem. Biophys. Res. Commun. 198:597-604(1994).
 RN [6]
 RP SEQUENCE OF 21-371.
 RX MEDLINE=91131556; PubMed=1993651;
 RA Lee Y.-M., Leiby K.R., Allar J., Paris K., Lerch B., Okarma T.B.;
 RT "Primary structure of bovine conglutinin, a member of the C-type
 animal lectin family.";
 RL J. Biol. Chem. 266:2715-2723(1991).
 RN [7]
 RP PRELIMINARY SEQUENCE OF 21-52.
 RX MEDLINE=87184551; PubMed=3566740;
 RA Young N.M., Leon M.A.;
 RT "The carbohydrate specificity of conglutinin and its homology to
 proteins in the hepatic lectin family.";
 RL Biochem. Biophys. Res. Commun. 143:645-651(1987).
 CC -!- FUNCTION: Calcium-dependent lectin-like protein which binds to a
 yeast cell wall extract and immune complexes through the
 complement component (C3bi). It is capable of binding nonreducing
 terminal N-acetylglucosamine, mannose and fucose residues.
 CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
 CC -!- SIMILARITY: Contains 1 collagenous domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 DR EMBL; D14085; BAA03170.1; -
 DR EMBL; X71774; CAA50565.1; -
 DR EMBL; L18871; AAR20126.1; -
 DR EMBL; U06860; AAB60624.1; -
 DR EMBL; U06854; AAB60624.1; JOINED.
 DR EMBL; U06855; AAB60624.1; JOINED.
 DR EMBL; U06856; AAB60624.1; JOINED.
 DR EMBL; U06857; AAB60624.1; JOINED.
 DR EMBL; U06858; AAB60624.1; JOINED.
 DR EMBL; U06859; AAB60624.1; JOINED.
 DR EMBL; D25302; BAA04983.2; -
 DR EMBL; D25296; BAA04983.2; JOINED.
 DR EMBL; D25297; BAA04983.2; JOINED.
 DR EMBL; D25298; BAA04983.2; JOINED.
 DR EMBL; D25299; BAA04983.2; JOINED.
 DR EMBL; D25300; BAA04983.2; JOINED.
 DR EMBL; D25301; BAA04983.2; JOINED.
 DR PIR; I45878; I45878.
 DR PIR; JN0450; JN0450.
 DR HSSP; P35247; 1B08.
 DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.

R InterPro; IPR001304; Lectin_C.
R Pfam; PF01391; Collagen; 3.
R Pfam; PF00059; lectin_C.1.
R ProDom; PD000007; Cig_helix; 1.
R SMART; SM00034; CLECT; 1.
R PROSITE; PS00615; C-TYPE LECTIN 1; 1.
R PROSITE; PS00041; C-TYPE LECTIN 2; 1.
R Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane;
R Collagen; Repeat; Calcium; Signal.
I SIGNAL 1 20
I CHAIN 21 371
I DOMAIN 46 216
I MOD_RES 273 371
I MOD_RES 63 63
I MOD_RES 87 87
I MOD_RES 99 99
I MOD_RES 135 135
I MOD_RES 141 141
I MOD_RES 159 159
I MOD_RES 162 162
I MOD_RES 198 198
I SITE 201 203
I DISULFID 275 369
I DISULFID 347 351
I CARBOHYD 337 337
I CONFLICT 173 173
I CONFLICT 210 210
I CONFLICT 218 218
I CONFLICT 272 272
I CONFLICT 272 272
I SEQUENCE 371 AA; 37994 MW; 867BBA1992544B1F CRC64;
Query Match 22.1%; Score 328.5; DB 1; Length 371;
Best Local Similarity 29.5%; Pred. No. 1.2e-20;
Matches 85; Conservative 35; Mismatches 95; Indels 73; Gaps 10;
Y 46 PGKGGDGGKGP-----GEEGKKGKVGMPGKIGKELGDMGDRGNICK-----TGP 93
b 96 PGKGTGTGRPGMPGAPRGPSKQSGMGPPTPGKGTGKGVGAPGIGQFPG 155
Y 94 IGKKGKSGKLLGIPGE-----KGKAG- 116
b 156 SGLKGEKAPGETGAPGAGVTPGSAIGPQPGFSGARGPGLKGRDGPBTGAKGSSGL 215
Y 117 -----TVCCGRYKFKVQGLDISARLKTSMKVNVIAGIRETEKFFVIQEE 166
b 216 AYNALKQRTVILD-GLHRRFN-----AFSQYKAVLPDQAVG-----EKIKTAGAV 265
Y 167 KNYRESLTHIRGGMAMPKDEAAANTLIADYVAKSGFFRVIGVNDLEREGYQNTDNT 226
b 266 KSYSDAEQLCREAKQLASPRSAENAVTQMV-RAQEKNAVLSNNDISTEGRTYPTGE 324
Y 227 PLQYNSNNEGEF--SDPYGHEDCVEMLSGGRWNTCHLTMYFVCEP 272
b 325 ILV-YSNWDGEPNNSDEQPCNCEVIFPDGKWNVPCKQLLVICEF 371
RESULT 8
SPA RABIT
D -PSPA RABIT STANDARD; PRT; 247 AA.
C P12842;
T 01-OCT-1989 (Rel. 12, Created)
T 01-OCT-1989 (Rel. 12, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
Y Pulmonary surfactant-associated protein A precursor (SP-A) (PSP-A) (PSP-A).
b (PSP-A).
N SFTPA1 OR SFTPA OR SFTPA.
N Cryptolagus curiculus (Rabbit).
X Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
X NCBI_TaxID=9986;
N [1]
P SEQUENCE FROM N.A.
X MEDLINE=88139348; PubMed=2830270;

Boggaram V., Qing K., Mendelson C.R.;
"the major apoprotein of rabbit pulmonary surfactant. Elucidation of primary sequence and cyclic AMP and developmental regulation.";
J. Biol. Chem. 263:2939-2947(1988).
(2)
RN SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=92312742; PubMed=1616051;
RA Chen Q., Boggaram V., Mendelson C.R.;
"Rabbit lung surfactant protein A gene: identification of a lung-specific DNase I hypersensitive site";
Am. J. Physiol. 262:L662-L671(1992).
CC -!- FUNCTION: In presence of calcium ions, PSAP binds to surfactant phospholipids and contributes to lower the surface tension at the air-liquid interface in the alveoli of the mammalian lung and is essential for normal respiration.
CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10% protein. There are 4 surfactant-associated protein: 2 collagenous, carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small hydrophobic proteins (SP-B and SP-C).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC EMBL; J03542; AAA31465.1; -
DR EMBL; L19387; AAA31468.1; -
DR PIR; A29931; LNRBPS.
DR HSP; P22897; 1EGG.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; lectin_C.1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Glycoprotein; Calcium; Surface Film; Gaseous exchange; Hydroxylation; Signal; Lectin; Collagen; Repeat.
FT SIGNAL 1 15
FT CHAIN 16 247
FT POTENTIAL.
FT PULMONARY SURFACTANT-ASSOCIATED PROTEIN A.
FT DOMAIN 27 99
FT C-TYPE LECTIN (SHORT FORM).
FT DISULFID 152 247
FT DISULFID 154 245
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (PROBABLE).
FT S -> P. APWA (IN REF. 2).
FT VARIANT 12 12
FT CONFLICT 57 60
FT SEQUENCE 247 AA; 26071 MW; 289634054C8C8B4 CRC64;
Query Match 20.6%; Score 305.5; DB 1; Length 247;
Best Local Similarity 31.2%; Pred. No. 6.9e-19;
Matches 85; Conservative 30; Mismatches 104; Indels 53; Gaps 9;
QY 25 SGLGIDSRPRAEVCATHTI---SPGKGGDGEKDPGCEGKGVGMGPKGKIGLGD 81
Db 5 SLALTLSAPASDTCOTKDVCGISGPGIFGTFGSLGDPGRDGVGDPGPPGPPGG 64
QY 82 M-----GDRGNICKTPIGKGDGKGLLGI;PGKKGAGTVCDCGRYKFFVGLD----- 132
Db 65 MPGLPGRDGLICAPGVGEGDKCE-----PGEKGGP-----LPAYLDEELQA 108
QY 133 -----ISARLKTSMKFNVIAGIRETEKFFVIQEEKRYRESLTHCHIRG 180
Db 109 TLHLRHHALQISGLVLSQSGMKAV-----GKIFSTNGQSVNFDAIREVCARAG 158


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QY 181 GVLAMPKDEAANTLIADYVAKSGFRFVIGVNDLERSCQWFTDNTPLONYSWNGERS 240
Db 159 GRIAVPRSLRENEAIASVSKERNY-AYGLAEGTAGDFYLDGDEV-NYTNWYFGEPR 216
QY 241 DRYGHEDCEVEMLSGRWMDTECHLTMFVCFE 272
Db 217 G-QGKEKCVMTYDGKNDKNCLOVRLVCFE 247

RESULT 9
MABA_RAT
ID MABA_RAT STANDARD; PRT; 238 AA.
AC P19999;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-WAR-2004 (Rel. 43, Last annotation update)
DE Mannose-binding protein A precursor (MBP-A) (Mannan-binding protein).
GN MBP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=86196130; PubMed=3009480;
RA Drickamer K., Dordal M.S., Reynolds L.;
RT "Mannose-binding proteins isolated from rat liver contain
carbohydrate-recognition domains linked to collagenous tails.
Complete primary structures and homology with pulmonary surfactant
apoprotein.";
RL J. Biol. Chem. 261:6878-6887(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=87137502; PubMed=3029088;
RA Drickamer K., McCreary V.;
RT "Exon structure of a mannose-binding protein gene reflects its
evolutionary relationship to the asialoglycoprotein receptor and
nonfibrillar collagens.";
RL J. Biol. Chem. 262:2582-2589(1987).
RN [3]
RP SEQUENCE OF 18-42.
RX MEDLINE=87222358; PubMed=3584121;
RA Ikeda K., Sannoh T., Kawasaki N., Kawasaki T., Yamashina I.;
RT "Serum lectin with known structure activates complement through the
classical pathway.";
RL J. Biol. Chem. 262:7451-7454(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 124-238.
RX MEDLINE=92086855; PubMed=1721241;
RA Weis W.I., Kahn R., Fourme R., Drickamer K., Hendrickson W.A.;
RT "Structure of the calcium-dependent lectin domain from a rat mannose-
binding protein determined by MAD phasing.";
RL Science 254:1608-1615(1991).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 124-238.
RX MEDLINE=93063338; PubMed=1436090;
RA Weis W.I., Drickamer K., Hendrickson W.A.;
RT "Structure of a C-type mannose-binding protein complexed with an
oligosaccharide.";
RL Nature 360:127-134(1992).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 84-238.
RX MEDLINE=95219384; PubMed=7704532;
RA Weis W.I., Drickamer K.;
RT "Trimeric structure of a C-type mannose-binding protein.";
RL Structure 2:1227-1240(1994).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 90-238.
RX MEDLINE=99119227; PubMed=9922165;
RA Ng K.K.-S., Park-Snyder S., Weis W.I.;

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RT "Ca2+-dependent structural changes in C-type mannose-binding
proteins.";
RL Biochemistry 37:17965-17976(1998).
CC -!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-
dependent manner. Is capable of host defense against pathogens, by
activating the classical complement pathway independently of the
antibody.
CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
CC -!- SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MOST
PREDOMINANTLY IN THE ROUGH ENDOPLASMIC RETICULUM AND IN THE GOLGI
APPARATUS, AND LITTLE OR NO MBP IS PRESENT IN PLASMA MEMBRANES AND
LYSOSOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNA SPACE
OF THE ORGANELLES, PROBABLY AS A LOOSELY BOUND MEMBRANE PROTEIN.
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M14105; AAA98781.1; ..
CC EMBL; M14104; AAA98781.1; JOINED.
CC PIR; S24791; LNETMA.
CC PDB; 1MSB; 15-JAN-92.
CC PDB; 2MSB; 31-OCT-93.
CC PDB; 1AFA; 03-APR-96.
CC PDB; 1AFB; 03-APR-96.
CC PDB; 1AFD; 03-APR-96.
CC PDB; 1ATM; 07-FEB-95.
CC PDB; 1KMB; 12-FEB-97.
CC PDB; 2KMB; 12-FEB-97.
CC PDB; 3KMB; 12-FEB-97.
CC PDB; 4KMB; 12-FEB-97.
CC PDB; 1YTT; 10-JUN-96.
CC PDB; 1BCH; 17-JUN-98.
CC PDB; 1BCU; 17-JUN-98.
CC PDB; 1BUU; 09-SEP-99.
CC PDB; 1FIF; 10-JAN-01.
CC PDB; 1FIH; 10-JAN-01.
CC PDB; 1KWT; 05-JUL-02.
CC PDB; 1KWU; 05-JUL-02.
CC PDB; 1KWV; 05-JUL-02.
CC PDB; 1KWX; 05-JUL-02.
CC PDB; 1KWX; 05-JUL-02.
CC PDB; 1KXZ; 05-JUL-02.
CC PDB; 1KX0; 05-JUL-02.
CC PDB; 1KX1; 05-JUL-02.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF01391; Collagen; 1.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN 1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;
Signal; Collagen; Lectin; Glycoprotein; Hydroxylation; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 238 MANNOSE-BINDING PROTEIN A.
FT DOMAIN 39 88 COLLAGEN-LIKE.
FT DOMAIN 143 238 C-TYPE LECTIN (SHORT FORM).
FT MOD_RES 43 43 HYDROXYLATION (POTENTIAL).
FT MOD_RES 61 61 HYDROXYLATION.
FT MOD_RES 67 67 HYDROXYLATION.
FT MOD_RES 73 73 HYDROXYLATION.
FT MOD_RES 78 78 HYDROXYLATION (POTENTIAL).
FT DISULFID 145 234
FT DISULFID 212 226
FT CONFLICT 156 156 R -> K (IN REF. 2).

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T HELIX 91 119
T TURN 120 121
T TURN 124 125
T STRAND 128 136
T HELIX 138 147
T TURN 148 149
T STRAND 151 152
T HELIX 158 168
T STRAND 172 177
T TURN 182 183
T STRAND 186 187
T TURN 188 189
T STRAND 192 192
T STRAND 198 198
T TURN 200 201
T TURN 207 208
T STRAND 212 215
T TURN 217 218
T STRAND 221 224
T TURN 226 227
T STRAND 230 236
T SEQUENCE 238 AA; 25308 MW; 1A927482B8A8CB3D CRC64;

Query Match 19.5%; Score 290; DB 1; Length 238;
Best Local Similarity 28.7%; Pred No. 1,4e-17;
Matches 75; Conservative 49; Mismatches 105; Indels 32; Gaps 8;

Y 14 ILVLFLQIQSLGDLIDSRPAEVCATHTISPPKGGDDGKGPGBEGKHGKVRGPKX 73
b 6 LLVLLCVSVSSGSGQ-TCEETLKTCS-VIACGRDGRDGPGRKGPQQ-----GLR 55
Y 74 GIKGELGMDGRNIGTPIGKKGKGEKGLGTPGKGRAGTVCDGRYKRFVGOLDI 133
b 56 GLOGPPGKLGPGVSGVAPSGQPKGQKGRG-----DSRAIEVKLANVEA 100
Y 134 SIARLKTSMKFKVKNVIAGI--RETEEFYIVQEEKYRESLTHCRINGGMLAMPKDEAA 191
b 101 EINTLKSLELTWKLHAFSGMKSGKGFVTHHERMPFSKVKALCSELGRGTVAIPTNAEE 160
Y 192 NTLIADYVAKSGFRFVIGVNDLEREGQYMPFDNTPLQYNSWNEGEPSDPYGHEDCVEM 251
b 161 NKAIQE-VAKTS---AFLGITDEVTEGQPMYVTGRL--TYSNWKKDEPNHGSGEDCVTI 215
Y 252 LSSGRWNDECHLTMTYFVCEP 272
b 216 VDNLGNLWDISQASHATVCEP 236

RESULT 10
ABC MOUSE STANDARD; PRT; 244 AA.
C P41317;
T 01-FEB-1995 (Rel. 31, Created)
T 01-FEB-1996 (Rel. 33, Last sequence update)
T 15-MAR-2004 (Rel. 43, Last annotation update)
E Mannose-binding protein C precursor (MBP-C) (Mannan-binding protein)
E (2A-reactive factor P28A subunit) (RARF/P28A).
E N MBL2.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
[1]
P SEQUENCE FROM N.A.
STRAIN=CBA/J; TISSUE=Liver;
MEDLINE=91302823; PubMed=1712818;
A Sastry K., Zahedi K., Lelias J.M., Whitehead A.S., Ezekowitz R.A.;
T "Molecular characterization of the mouse mannose-binding proteins.
T The mannose-binding protein A but not C is an acute phase reactant.";
L J. Immunol. 147:692-697(1991).
[2]
N SEQUENCE FROM N.A.
P STRAIN=BALB/c;

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RX MEDLINE=95284466; PubMed=7766991;
RA Sastry R., Wang J.S., Brown D.C., Ezekowitz R.A., Tauber A.I.,
RA Sastry K.N.;
RT "Characterization of murine mannose-binding protein genes Mb11 and
RT Mb12 reveals features common to other collectin genes.";
RL Mamm. Genome 6:103-110(1995).
[3]
RP SEQUENCE FROM N.A.
RA Kuge S., Ihara S., Watanabe E., Watanabe M., Takishima K., Suga T.,
RA Mamaiya G., Kawakami M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schain J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC -!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-
CC dependent manner. Is capable of host defense against pathogens, by
CC activating the classical complement pathway independently of the
CC antibody.
CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers
CC -!- SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MOST
CC PREDOMINANTLY IN THE ROUGH ENDOPLASMIC RETICULUM AND IN THE GOLGI
CC APPARATUS. AND LITTLE OR NO MBP IS PRESENT IN PLASMA MEMBRANES AND
CC LYSOSOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNA
CC SPACE OF THE ORGANELLES, PROBABLY AS A LOOSELY BOUND MEMBRANE
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC EMBL; S42294; AAB19343.1; -
CC EMBL; U09016; AAB2010.1; -
CC EMBL; U09013; AAB2010.1; JOINED.
CC EMBL; U09014; AAB2010.1; JOINED.
CC EMBL; U09015; AAB2010.1; JOINED.
CC EMBL; D11440; BAA02005.1; -
CC EMBL; BC010760; AAH10760.1; -
CC EMBL; I48651; LNM5MG.
CC FTR; I48651; 1RDO.
CC HSSP; P08661; 1RDO.
CC MGD; MGI:96924; Mb12.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR01304; Lectin_C.
CC Pfam; PF01391; Collagen; 1.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.

```


L Nat. Genet. 2:50-55(1992).
N [13]
P VARIANTS CYS-52; ASP-54 AND GLU-57.
X MEDLINE=99374928; PubMed=10447262.
A Gabolde M., Muralitharan S., Besmond C.;
T Genotyping of the three major allelic variants of the human
T mannose-binding lectin gene by denaturing gradient gel
T electrophoresis.;
L Hum. Mutat. 14:80-83(1999).
C -1- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-
C dependent manner. Is capable of host defense against pathogens,
C by activating the classical complement pathway independently of
C the antibody.
C -1- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
C -1- DISEASE: There is an association between low levels of MBL2 and a
C defect of opsonization which results in susceptibility to frequent
C and chronic infections.
C -1- SIMILARITY: Contains 1 collagenous domain.
C -1- SIMILARITY: Contains 1 C-type lectin family domain.
C -1- CAUTION: There are extensive differences between the revised
C sequence in Ref.1 and that published in Ref.2.
C -----
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C or send an email to license@isb-sib.ch).
C -----
R EMBL; X15422; CAA33462.1; -
R EMBL; X15954; CAA34079.1; -
R EMBL; X15955; CAA34079.1; JOINED.
R EMBL; X15955; CAA34079.1; JOINED.
R EMBL; X15957; CAA34079.1; JOINED.
R EMBL; AF080510; AAC31937.1; -
R EMBL; AF080508; AAC31937.1; JOINED.
R EMBL; AF080509; AAC31937.1; JOINED.
R EMBL; Y16576; CAB56044.1; -
R EMBL; Y16577; CAB56120.1; -
R EMBL; Y16578; CAB56045.1; -
R EMBL; Y16579; CAB56121.1; -
R EMBL; Y16580; CAB56122.1; -
R EMBL; Y16581; CAB56123.1; -
R EMBL; Y16582; CAB56124.1; -
R EMBL; AF360991; AAK52907.1; -
R EMBL; AF482699; AAN39274.1; -
R EMBL; AF482700; AAN39275.1; -
R PIR; JLO115; LNHUNC.
R PDB; 1HUP; 15-OCT-95.
R Genew; HGNC:6922; MBL2.
R MIM; 154545; -
R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0003793; F:defense/immunity protein activity; TAS.
R GO; GO:0008955; P:immune response; TAS.
R InterPro; IPR008160; Collagen.
R InterPro; IPR001304; Lectin_C.
R Pfam; PF01391; Collagen; 1.
R Pfam; PF00059; Lectin_c; 1.
R SMART; SMC0034; CLECT; 1.
R PROSITE; PS00615; C-TYPE LECTIN 1; 1.
R PROSITE; PS50041; C-TYPE LECTIN 2; 1.
W Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;
W Signal; Collagen; Lectin; Glycoprotein; Hydroxylation; Polymorphism;
W 3D-structure.
T CHAIN 1 20
T CHAIN 21 248
T DOMAIN 21 41
T DOMAIN 42 99
T DOMAIN 134 245
T MOD_RES 47 47
T MOD_RES 73 73
T MOD_RES 79 79
T MOD_RES 79 79

FT MOD_RES 82 82 HYDROXYLATION.
FT MOD_RES 88 88 HYDROXYLATION.
FT DISULFID 155 244
FT DISULFID 222 236
FT VARIANT 24 24
FT VARIANT 52 52
FT VARIANT 54 54
FT VARIANT 57 57
FT TURN 109 109
FT HELIX 110 129
FT TURN 130 130
FT STRAND 132 134
FT TURN 135 136
FT STRAND 137 147
FT HELIX 148 157
FT TURN 158 159
FT STRAND 161 162
FT HELIX 168 177
FT STRAND 182 187
FT TURN 192 193
FT STRAND 196 197
Query Match 19.5%; Score 289.5; DB 1; Length 248;
Best Local Similarity 31.1%; Pred. No. 1.6e-17;
Matches 75; Conservative 37; Mismatches 100; Indels 29; Gaps 7;
QY 34 PTAEVCAHTTIS--PGPKGDDGEGKDFGEGGKGVGRMGPKGIKGLGDMGRGNIGKT 91
DB 33 PAVIACSSPGINGPFKDGDRDGTGKGEFGQ-----GLRGLQGGPPGKLGPPGPGPS 85
QY 92 GTIGKKGDKGKGLLIGIPGEGKAGTVCDCGRVYKFGVQLDIDISTARLKTSMKFTVGNVIAG 151
DB 86 GSPGPKGQKDPG-----KSPGDSLSLAASEK---ALQTEWARIKKWLTSLG---- 131
QY 152 IRETEEKFYIVQBEKNYRESLTHCRIRGGMAMPKDEAANTLIADYVAKSGFRVFIGV 211
DB 132 -KQGVNKFELTNGEIMTFEKVKALCVFQASVATPRNAENGAIONLIKE----EAPLGI 186
QY 212 NDLEEGGYMFTDNTPLQVSNWNEGPPSDPYGHEDCVEMLSGRWNTDTEHLTMYFVCE 271
DB 187 TDEKTEGQFVLDLTGNRL--TYTNWNEGPNAGSDSDCVLLKKGQWNVPCSTSHLAVCE 245
QY 272 F 272
DB 246 F 246
RESULT 12
PSPA_PIG STANDARD; PRT; 249 AA.
ID PSPA_PIG
AC P49874;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pulmonary surfactant-associated protein A precursor (SP-A) (PSP-A)
DE (PSPAP).
GN SFTPA1 OR SFTPA OR SFTP1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Adamou J.E., Elshourbagy N.A.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: In presence of calcium ions, PSAP binds to surfactant
CC phospholipids and contributes to lower the surface tension at the
CC air-liquid interface in the alveoli of the mammalian lung and is
CC essential for normal respiration.
CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
CC protein. There are 4 surfactant-associated protein: 2 collagenous,
CC carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small
CC hydrophobic proteins (SP-B and SP-C) (By similarity).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L41350; AAA88403.1; --
CC HSSP; P22897; LECS.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR001304; Lectin C.
CC Pfam; PF01391; Collagen; 2.
CC Pfam; PF00059; lectin c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN 1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN 2; 1.
CC Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
CC Signal; Lectin; Collagen; Repeat.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 249 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
CC A.
CC DOMAIN 28 100 COLLAGEN-LIKE.
CC DOMAIN 153 249 C-TYPE LECTIN (SHORT FORM).
CC DISULFID 155 247 BY SIMILARITY.
CC DISULFID 225 239 BY SIMILARITY.
CC CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 249 AA; 26702 MW; 3C4E05AD07F2A7CD CRC64;
CC -----
CC Query Match 19.2%; Score 285.5; DB 1; Length 249;
CC Best Local Similarity 31.2%; Pred No. 3.5e-17;
CC Matches 85; Conservative 35; Mismatches 111; Indels 41; Gaps 12;
QY 14 ILVLFLQIQSLGIDISRPTAEVCATHITSPGKGDGKDPGEGKHGKVGKRGPK 73
Db . 6 LAUTFLLAVSLGCDV-----KEVCLA---SPGTPGTGSHGLPGRDGRGDKGDPGPP 57
QY 74 GIKGELGMDGRGNIGTKGPIGKGDKEKGLGIPGKKGAGTVCDCGRYKRVGQLDI 133
Db 58 GPMGPPGVA--GPPQDGMIGAPLPGERKEGEPGPPG-----LPAHLD- 104
QY 134 SIARLKTSMKFKVNI---AGIRETEEFYIVQEKNYRE-----SLTHC-RIRG 190
Db 105 --EELQSALEHTRHQILQSMGVLSFQE--FMLAVGEKVFSTNGQSVAFMWSLSCVPEQV 160
QY 181 GMLAMPKDBAANTLADYVAKSGFRFRVIGVNDLEREQYMTDTNTLQNYNNWNEGERS 240
Db 161 GRIAAPRSPENEAASIVKKNIT-AYLVGVEGPTAGDFYLDGTEV-NYTNWYCEPR 218
QY 241 DPYGHEDCVMELSSGRWMDTECHLTMYVCEPF 272
Db 219 G-RGKEKCVMTDQWDRNCQQVRLAICEF 249
RESULT 13
MABC_BOVIN STANDARD; PRT; 249 AA.
AC C02659;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mannose-binding protein C precursor (MBP-C) (Mannan-binding protein).
GN MBL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=97228413; PubMed=9074491;
RA Kawai T., Suzuki Y., Eda S., Ohtani K., Kase T., Fujinaga Y.,
RT "Cloning and characterization of a cDNA encoding bovine mannan-binding
RT protein.";
RL Gene 186:161-165(1997).
CC -!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-
CC dependent manner. Is capable of host defense against pathogens, by
CC activating the classical complement pathway independently of the
CC antibody (By similarity).
CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D73408; BAA18935.1; --
CC HSSP; P11226; LHUP.
CC InterPro; IPR008161; Clq helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR001304; Lectin C.
CC Pfam; PF01391; Collagen; 1.
CC Pfam; PF00059; lectin c; 1.
CC ProDom; PD000007; Clq_helix; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN 1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN 2; 1.
CC Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;
CC Signal; Collagen; Lectin; Glycoprotein; Hydroxylation.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 249 MANNOSE-BINDING PROTEIN C.
CC DOMAIN 43 101 COLLAGEN-LIKE.
CC DOMAIN 135 246 C-TYPE LECTIN.
CC MOD RES 48 48 HYDROXYLATION (POTENTIAL).
CC MOD RES 63 63 HYDROXYLATION (POTENTIAL).
CC MOD RES 74 74 HYDROXYLATION (POTENTIAL).
CC MOD RES 83 83 HYDROXYLATION (POTENTIAL).
CC MOD RES 86 86 HYDROXYLATION (POTENTIAL).
CC DISULFID 34 34 INTERCHAIN (BY SIMILARITY).
CC DISULFID 39 39 INTERCHAIN (BY SIMILARITY).
CC DISULFID 156 245 BY SIMILARITY.
CC DISULFID 223 237 BY SIMILARITY.
CC SEQUENCE 249 AA; 26471 MW; 29FC9F5927A66DD5 CRC64;
CC -----
CC Query Match 19.2%; Score 284.5; DB 1; Length 249;
CC Best Local Similarity 34.5%; Pred. No. 4.2e-17;
CC Matches 77; Conservative 31; Mismatches 94; Indels 21; Gaps 8;
QY 56 GDPGEGKHGKVGKIPGKIGKELGMDGRGNIGTKGPIGKGDKEKGLGIP---GEK 112
Db 40 GPPGINGIPGKDGKDGAKGKGEFG----QELRSGQPPGKGGPQGTPIGPIGPIGK 95
QY 113 GKAGTVCDCGRYKRVGQLDISIRLKTSMKFKVNI---VIAGIRETEEFYIVQEKNYR 170
Db 96 GDPGE--NMGDYIRLATS----ERATLQSELNQIKNWLIFSLGKRVGKGAFFNGKMPEN 150

Y 171 ESLTHCRIRGMLAMPKDAANTLIADYVAKSGPRFVIGVNDLEREGQYMTDNTPL-Q 229
b 151 EVKTLCAQOGRVATPMNAEENRALKDLVTE----EALGIDTQTEGK--FVDLTGKGV 204
Y 230 NYSNNWNEGSPDPYGHEDCVEMLSRGRNDTECHLTMTYFVCEP 272
b 205 TYQWNWDGEPNNASPGCHVCVTLLSDGTWNDIACSASFVTVCEP 247

RESULT 14
SPA_HUMAN STANDARD; PRT; 248 AA.
C P07714;
T 01-APR-1988 (Rel. 07, Created)
T 01-APR-1990 (Rel. 14, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Pulmonary surfactant-associated protein A precursor (SP-A) (PSP-A)
E (PSPAP) (Alveolar proteinosis protein) (35 kDa pulmonary surfactant-
E associated protein).
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
N SEQUENCE FROM N.A.
P MEDLINE=86250832; PubMed=3755136;
X A Flores J., Steinbrink R., Jacobs K., Phelps D., Kriz R., Rechy M.,
A Sultman L., Jones S., Teusch H.W., Frank H.A., Fritsch E.F.,
T "Isolation and characterization of cDNA clones for the 35-kDa
L J. Biol. Chem. 261:9029-9033(1986).
N [2]
N SEQUENCE FROM N.A.
P MEDLINE=86014366; PubMed=2995821;
X A White R.T., Damm D., Miller J., Spratt K., Schilling J., Hawgood S.,
A Benson B., Cordell B.,
T "Isolation and characterization of the human pulmonary surfactant
T apoprotein gene.";
L Nature 317:361-363(1995).
N [3]
N SEQUENCE FROM N.A.
P MEDLINE=92198680; PubMed=1372511;
X Katyal S.L., Singh G., Locker J.L.,
A "Characterization of a second human pulmonary surfactant-associated
T protein SP-A gene.";
L Am. J. Respir. Cell Mol. Biol. 6:446-452(1992).
C -I- FUNCTION: In presence of calcium ions, PSAP binds to surfactant
C phospholipids and contributes to lower the surface tension at the
C air-liquid interface in the alveoli of the mammalian lung and is
C essential for normal respiration.
C -I- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
C -I- SUBCELLULAR LOCATION: Extracellular.
C -I- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
C protein. There are 4 surfactant-associated protein: 2 collagenous,
C carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small
C hydrophobic proteins (SP-B and SP-C).
C -I- SIMILARITY: Contains 1 collagenous domain.
C -I- SIMILARITY: Contains 1 C-type lectin family domain.
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C or send an email to license@isb-sib.ch).
R EMBL; M13686; AAA60211.1; -
R EMBL; M33475; AAA36520.1; -
R EMBL; M30838; AAA36510.1; -
R EMBL; M68519; AAA60319.1; -
R PIR; A25720; LNHUP6.

HSP; P22897; IEGG.
Genew; HGNC:10798; SFTPA1.
Genew; HGNC:10799; SFTPA2.
DR MIM; 178630; -
DR MIM; 178642; -
DR GO; GO:0005319; F:lipid transporter activity; TAS.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Glycoprotein; Calcium; Surface Film; Gaseous exchange; Hydroxylation;
KW Signal; Lectin; Collagen; Repeat; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 248 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
FT A.
FT DOMAIN 28 100 COLLAGEN-LIKE.
FT DOMAIN 153 248 C-TYPE LECTIN (SHORT FORM).
FT DISULFID 155 246 BY SIMILARITY.
FT DISULFID 224 238 BY SIMILARITY.
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (PROBABLE).
FT VARIANT 9 9 N -> T.
FT VARIANT 50 50 /FTID=VAR_004184.
FT VARIANT 66 66 L -> V.
FT VARIANT 73 73 /FTID=VAR_012231.
FT VARIANT 81 81 M -> T.
FT VARIANT 85 85 /FTID=VAR_004185.
FT VARIANT 219 219 D -> N.
FT VARIANT 81 81 /FTID=VAR_004186.
FT VARIANT 85 85 I -> V.
FT VARIANT 219 219 /FTID=VAR_004187.
FT VARIANT 223 223 C -> R.
FT VARIANT 19 19 /FTID=VAR_004188.
FT VARIANT 223 223 R -> W.
FT VARIANT 19 19 /FTID=VAR_012232.
FT VARIANT 45 45 Q -> K.
FT VARIANT 54 54 /FTID=VAR_012233.
FT VARIANT 91 91 A -> V (IN REF. 2).
FT VARIANT 100 100 D -> H (IN REF. 2).
FT VARIANT 247 247 P -> L (IN REF. 2).
FT VARIANT 247 247 P -> A (IN REF. 3).
FT VARIANT 247 247 P -> R (IN REF. 2).
FT VARIANT 247 247 E -> D (IN REF. 3).
SQ SEQUENCE 248 AA; 26214 MW; 6A9F0C3488BF3633 CRC64;
Query Match 19.1%; Score 284; DB 1; Length 248;
Best Local Similarity 29.9%; Pred. No. 4.6e-17;
Matches 78; Conservative 42; Mismatches 119; Indels 22; Gaps 9;
QY 16 LVLFLLQSLGLDIDSRPTAEVCATHTISPGKDDGKDPCEGKHKVGMGPKGI 75
Db 6 LALNLTMAASGAACEVK---DVCVG---SPGIPGTGSHGLPGDRGRDGLKGDGPPGP 59
QY 76 KGEIDMG-DRGNIGKTGPIGKKGDKGKGLLGLPGKKGAGTVCDGGRYKFKVGQLDIS 134
Db 60 MGPPGEMCPGNDGLPCAPGIPGEGEK---GEPGERGPPGLPAHLDE-----ELQAT 110
QY 135 IARLTKSMKFKVKNVIA---GIRETEKPYIVQEKYRESLTHCRIRGMLAMPKDEAA 191
Db 111 LHDFRHLQIOTRGALSLOGSINTVGEKVFSSNGOSITFDAIQEACARAGRIAPRNPPEE 170
QY 192 NTLIADYVAKSGFFRVFVGVNDLEREGQYMTDNTPLQYNNWNEGFSPPYGHEDCVEM 251
Db 171 NEALASFVKKNTY-AYVGLTEGSPGDFRISDGTVP-NYTNWYRGEPAG-RGKEQCVEM 227
QY 252 LSSGRWNTECHLTMTYFVCEP 272
Db 228 YTDGQWNRNCLYSRLTICEF 248

RESULT 15

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: February 24, 2004, 02:10:36 ; Search time 28 Seconds
(without alignments)
951.609 Million cell updates/sec

file: US-09-600-932-2
effect score: 1484
sequence: 1 MNGFASLLRRNQFILLVLF.....NDTECHLTMYFVCFIKKK 277

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues
total number of hits satisfying chosen parameters: 283366

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	ID	Description
1	1318	88.8	277	JC7903	collectin liver 1
2	352.5	23.8	369	S33603	surfactant protein
3	345	23.2	301	A53570	collectin-43 - bov
4	337	22.7	375	A45225	pulmonary surfacta
5	333	22.4	374	A42046	surfactant protein
6	328.5	22.1	371	UN0450	conglutinin precur
7	328.5	22.1	371	I45878	conglutinin - bovi
8	305.5	20.6	247	LNRP85	pulmonary surfacta
9	290	19.5	238	LNRTMA	mannose-binding le
10	290	19.5	244	LNMSMC	mannose-binding le
11	289.5	19.5	248	LNHUMC	mannose-binding le
12	287	19.3	248	LNHUP1	pulmonary surfacta
13	285.5	19.2	248	LNHUPS	pulmonary surfacta
14	284.5	19.2	248	I51921	pulmonary surfacta
15	284	19.1	248	LNHUP6	pulmonary surfacta
16	280	18.9	248	LNDRPS	pulmonary surfacta
17	279	18.8	244	LNRTMC	mannose-binding le
18	277	18.7	248	LNRTPS	pulmonary surfacta
19	273	18.4	742	JC7595	scavenger receptor
20	270.5	18.2	239	LNW5MA	mannose-binding le
21	269.5	18.2	248	A49853	pulmonary surfacta
22	207	13.9	618	S32436	collagen alpha 2(I
23	205	13.8	645	D90782	probable tail fibe
24	205	13.8	645	H85642	probable tail fibe
25	203	13.7	688	A53330	collagen alpha 2(I
26	196	13.2	1775	A31893	collagen alpha 1(I
27	193	13.0	1549	I48103	type VII collagen
28	192.5	13.0	2944	A54849	collagen alpha 1(V
29	191.5	12.9	1366	CGHU25	collagen alpha 2(I

ALIGNMENTS

RESULT 1

JC7903
collectin liver 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:Accession: JC7903
R:Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuh, A.
Biocet. Biotechnol. Biochem. 66, 2134-2145, 2002
A:Title: Molecular cloning of mouse collectin liver 1.
A:Reference number: JC7903; PMID:22333927; PMID:12450124
A:Accession: JC7903
A:Molecule type: mRNA
A:Residues: 1-277 <KAW>
A:Cross-references: DDBJ:AB016429
A:Experimental source: liver
C:Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebr
c development.
C:Genetics:
A:Gene: C11l
A:Map position: 15

Query Match	88.8%	Score 1318;	DB 2;	Length 277;
Best Local Similarity	88.1%	Pred. No. 5.4e-102;		
Matches	244;	Conservative 12;	Mismatches 21;	Indels 0; Gaps 0;
QY	1	MNGFASLLRRNQFILLVLFLLQIQSLGIDIDSRPTARVCATHITISPGKGDGKGPGE	60	
Db	1	MNGFVLLRSNLSMLLLALLHFQSLGLDVDSRAAEVCATHITISPGKGDGGRGTGE	60	
QY	61	EGKHGKVGMPGKIGKELGDMGRNIGKTGPIGKKGDKGKGLLIGPKGKAGTVCD	120	
Db	61	EGKDKGVGRQGPVKVKGELGDMGAQGNIGKSGPIGKKGDKGKGLLIGPKGKAGTICD	120	
QY	121	CGRYKFKVQGLDISARLKTSMKFNKVNVIAGIRTEKFFYVQEEKVRESLTHCRIG	180	
Db	121	CGRYKFKVQGLDISVARLKTSMKIKNVIAGIRTEKFFYVQEEKVRESLTHCRIG	180	
QY	181	GMLAMPKORAAANTLIADYVAKSGFFRVPIGVNDRERGQYMTDTPLQYNNKEEPS	240	
Db	181	GMLAMPKDEVTNTLIADYVAKSGFFRVPIGVNDRERGQYVFTDTPLQYNNKEEPS	240	
QY	241	DPYGHEDCEVMLSSGRWNTDTECHLTMYFVCFEIKKK	277	
Db	241	DPFSGHEDCEVMLSSGRWNTDTECHLTMYFVCFEIKKK	277	

RESULT 2

S33603
surfactant protein D - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S33603

R;Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A/Title: Structural similarity between bovine conglutinin and bovine lung surfactant protein
A/Reference number: S33603; MUID:93170856; PMID:8436402
A/Accession: S33603
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-369 <LIM>
C/Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:128-367/Domain: C-type lectin homology <LCH>

Query Match 23.8%; Score 352.5; DB 2; Length 369;
Best Local Similarity 31.1%; Pred. No. 1e-21;
Matches 92; Conservative 36; Mismatches 109; Indels 59; Gaps 8;

QY 26 LGLDIDSRPTAECVATHITISPGFKGDDGKEDP-----GEGKHGKVGGM----- 70
DB 84 IGLKGDNGSAGE-----PGFKDTPGPPGPPGPGAGREGPGKQSGMPPGTPGPX 135
QY 71 -----GPKGIGKGLGDMGD-----RGNIGKTGPIGKKGDK 100
DB 136 GDTGPKGVGARGIQSGPGAGLKGKRGAPDGPAGPAGPGRGAGPGQSGGARGPP 195
QY 101 GEKGLLIGPGEKAGT--VDCGGRYKRVGQGLDISIARLKTSMKFKVN--VIAGIRETE 156
DB 196 GLKGDRTGEGKAGSGSLAEVNALRQVGLLEGQLRQLQAFQYKXAMLPNGRSVG 255
QY 157 EKFYIVVOEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLER 216
DB 256 EKIFKTVGSEKIFQDAQIQCTGAGQLSPRSGAGNEALTO-LATAQKAAFLMSBTRK 314
QY 217 EGQYMTDNTPLQYNNWNEGPSPFYGHEDCVEMLSGRWNTDTECHLTMYFVCEP 272
DB 315 EGTFTVPTGEPVAV-YSNWAPQEPNNDGSGENCVEIFFNGKWNKVCGEQRLVCEP 369

RESULT 3
A53570
collectin-43 - bovine
N/Alternate names: lectin CL-43
C/Species: Bos primigenius taurus (cattle)
C/Date: 12-Apr-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-1999
C/Accession: A53570; A46689
R;Lim, B.L.; Willis, A.C.; Reid, K.B.M.; Lu, J.; Laursen, S.B.; Jensenius, J.C.; Holmskov
J. Biol. Chem. 269, 11820-11824, 1994
A/Title: Primary structure of bovine collectin-43 (CL-43). Comparison with conglutinin
A/Reference number: A53570; MUID:94216283; PMID:8163480
A/Accession: A53570
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-301 <LIM>
A/Cross-references: GB:X75912
R;Holmskov, J.; Teisener, B.; Willis, A.C.; Reid, K.B.; Jensenius, J.C.
J. Biol. Chem. 268, 10120-10125, 1993
A/Title: Purification and characterization of a bovine serum lectin (CL-43) with structural
A/Reference number: A46689; MUID:93252891; PMID:8486682
A/Accession: A46689
A/Molecule type: protein
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-27 <HOL>
A/Experimental source: serum
A/Note: sequence extracted from NCBI backbone (NCBIF:131234)
C/Superfamily: pulmonary surfactant protein D; C-type lectin homology
C/Keywords: lectin
F:177-299/Domain: C-type lectin homology <LCH>

Query Match 23.2%; Score 345; DB 2; Length 301;
Best Local Similarity 35.0%; Pred. No. 3.4e-21;
Matches 86; Conservative 34; Mismatches 98; Indels 28; Gaps 8;

QY 45 SPQPKGDGDEKGPGE---GKHGKVGKMGPKGIGKGLGDMGDRGNIGTKTPIGKKGDKG 101
DB 56 SMQPPPTGPKGEPGEGGVGAPGPGSPGAPLKGKRGAPGPGGAGPGQGPSAMPPG 125

QY 102 EKGLLIGPGEKAG--TVCDGGRYKRVGQGLDISIARLKTSMKFKVNVIAGIRE----- 154
DB 126 LKGRDGPGEKAGGETSVLEVDTLRQRMENLEGEVQL-----ONIVTOYRKAVLFP 178
QY 155 ---TEEKFYIVQEEKYRESLTHCRIRGGMLAMPKDEAANTLIADYV-AKSGFFRVFI 209
DB 179 DGQAVGEKIFKTGAVASYSDAEQLCEEAGQLASPRSSAENEAVTQLVRANK--HAYL 236
QY 210 GVNDLERGQYMTDNTPLQYNNWNEGPSPD---PYGHEDCVEMLSGRWNTDTECHLTM 266
DB 237 SMNDISKEGKFTYPTGSL-DYSNWAPEPNNAKDEGPENCLEIYSDGNWNDIECREER 295
QY 267 YFVCEP 272
DB 296 LVICEP 301

RESULT 4
A45225
pulmonary surfactant protein D precursor - human
N/Alternate names: SP-D
C/Species: Homo sapiens (man)
C/Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 22-Jun-1999
A/Accession: A45225; S23434; S24555; S44420; S18382; A56776
R;Crouch, E.; Rust, K.; Veille, R.; Donis-Keller, H.; Grosso, L.
J. Biol. Chem. 268, 2976-2983, 1993
A/Title: Genomic organization of human surfactant protein D (SP-D). SP-D is encoded on
A/Reference number: A45225; MUID:93155122; PMID:8428971
A/Accession: A45225
A/Molecule type: DNA
A/Residues: 1-375 <CRO>
A/Cross-references: GB:L05483; GB:L05484; GB:L05485; NID:9292505; PIDN:AAB59450.1; PID:
A/Experimental source: placenta
A/Note: sequence extracted from NCBI backbone (NCBIF:124316)
R;Lu, J.; Willis, A.C.; Reid, K.B.M.
Biochem. J. 284, 795-802, 1992
A/Title: Purification, characterization and cDNA cloning of human lung surfactant prote:
A/Reference number: S23434; MUID:92322003; PMID:1339284
A/Accession: S23434
A/Molecule type: mRNA
A/Residues: 1-30, 'T', '123-179, 'A', '181-375 <LUJ1>
A/Cross-references: EMBL:X65018; NID:934766; PIDN:CAA46152.1; PID:g34767
A/Experimental source: lung
A/Accession: S24555
A/Molecule type: protein
A/Residues: 214-234, 'X', '236, 'XX', '239-241 <LUJ2>
R;Hoppe, H.J.; Barlow, P.N.; Reid, K.B.M.
FEBS Lett. 344, 191-195, 1994
A/Title: A parallel three stranded alpha-helical bundle at the nucleation site of colla:
A/Reference number: S44420; MUID:94244769; PMID:8187892
A/Accession: S44420
A/Molecule type: mRNA
A/Residues: 202-257 <HOP>
R;Rust, K.; Grosso, L.; Zhang, V.; Chang, D.; Persson, A.; Longmore, W.; Cai, G.Z.; Cron
Arch. Biochem. Biophys. 290, 116-126, 1991
A/Title: Human surfactant protein D: SP-D contains a C-type lectin carbohydrate recogni:
A/Reference number: S18382; MUID:91378578; PMID:1898081
A/Accession: S18382
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 'F', '60-205, 'P', '207-374, 'HF' <RUS>
A/Cross-references: GB:L05485; NID:9292505
A/Note: corrections to this sequence are reported in reference A56776
R;Crouch, E.; Persson, A.; Chang, D.
Am. J. Pathol. 142, 241-248, 1993
A/Title: Accumulation of surfactant protein D in human pulmonary alveolar proteinosis.
A/Reference number: A56776; MUID:93142849; PMID:8424457
A/Accession: A56776
A/Status: preliminary
A/Molecule type: protein
A/Residues: 46-58, 'F', '60-62, 'E', '64-72, 223-227, 'X', '229-239, 'P', '241-245, 'X', '247-256, 'X', '2:
A/Cross-references: PIDN:AAB25037.1; PID:9263973; PIDN:AAB25038.1; PID:g363974
A/Experimental source: bronchoalveolar lavage

;Note: sequence extracted from NCBI backbone (NCBIP:123024, NCBIP:123023); sequence modified
;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers the surface tension of the alveolar fluid.
;Comment: This protein is synthesized by alveolar type II cells.

;Genetics: GDB: SFTPD; SFTPD4; SP-D
;Cross-references: GDB:132674; OMIM:178635
;Map position: 10q22.2-10q23.1
;Superfamily: pulmonary surfactant protein D; C-type lectin homology
;Keywords: blocked amino end; calcium; glycoprotein; hydroxylysine; hydroxyproline; lung
;1-20/Domain: signal sequence #status predicted <SIG>
;21-375/Product: pulmonary surfactant protein D #status predicted <MAT>
;21-45/Domain: non-collagenous #status predicted <NC1>
;46-222/Domain: collagenous #status predicted <COL>
;223-375/Domain: non-collagenous #status predicted <NC2>
;254-373/Domain: C-type lectin homology <LCH>
;90/Binding site: carbohydrate (Asn) (covalent) #status predicted
;281-373,351-365/disulfide bonds: #status predicted

Query Match 22.7%; Score 337; DB 1; Length 375;
Best Local Similarity 35.2%; Pred. No. 2e-20;
Matches 86; Conservative 28; Mismatches 110; Indels 20; Gaps 6;
/ 46 PGKGGDCEKGPGEKGGKGVGRMPXGKIGELGDMGDRNICKTGPIGK----- 96
c 135 PGKGGDCEKGPGEKGGKGVGRMPXGKIGELGDMGDRNICKTGPIGK----- 96
y 97 ---KGDGKGGKGLGIPGEGKAGT--VDCGGRYKRFVQQLDISIARLKTSMKFFVKN--I 149
b 195 PGARPPGLKDGKIPGDKGAKGSLPDVASLRQVEALQGVQHLQAQSFYKVKELF 254
y 150 AGIRETEEFYVVOEKYRSLTHCIRGMLAMPKDEANLTIAD-VYAKSGFRVFI 209
b 255 PNGQSVGEKIFKTAGVRFVPTAQLLCTQAGGLASPRSAENALQVVAKNV--AAF 312
y 209 IGVDLEREGQVMTDNTPLQYNSNNEGEPSDPVGHEDCVEMLSGRWNTDECHLTMYF 269
b 313 LSTMDSKTEGKTYPTGESLV-YSNWAPEFNDGGSDCVEIFTGKWDNACGEQRLV 371
y 269 VCEF 272
b 372 VCEF 375
ESULT 5
42046
urfactant protein D - rat
;Species: Rattus norvegicus (Norway rat)
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
;Accession: A42046
;Shimizu, H.; Fisher, J.H.; Papet, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelker, D.R.
;Title: Primary structure of rat pulmonary surfactant protein D. cDNA and deduced amino acid sequence.
;Reference number: A42046; MUID:192112913; PMID:1370483
;Accession: A42046
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-374 <SHI>
;Cross-references: GB:M81231; NID:9207035; PIDN:AAA42170.1; PID:9207036
;Experimental source: lung
;Note: sequence extracted from NCBI backbone (NCBIN:76027, NCBIP:76031)
;Superfamily: pulmonary surfactant protein D; C-type lectin homology
;253-372/Domain: C-type lectin homology <LCH>

Query Match 22.4%; Score 333; DB 1; Length 374;
Best Local Similarity 32.1%; Pred. No. 4.e-20;
Matches 78; Conservative 36; Mismatches 111; Indels 18; Gaps 5;
y 46 PGKGGDCEKGPGEKGGKGVGRMPXGKIGELGDMGDRNICKTGPIGKGGKGE 102
b 134 PGKGGDCEKGPGEKGGKGVGRMPXGKIGELGDMGDRNICKTGPIGKGGKGE 193
y 103 KGLLGIPIGEGKAGTVCDCG-----RYRFFVGOLDISIAKLKTSMKFFVKN--VI 149

Db 194 PGRGPPGLKDGRCAPGDRGKIGESGLPDSALRQMEALNGKLRLAEAFSRYKKAALF 253
QY 150 AGIRETEEFYVVOEKYRSLTHCIRGMLAMPKDEANLTIAD-VYAKSGFRVFI 209
Db 254 PDGOSVGDKIPFRAANSEEPFEDAKEMCRQAGGLASPRSAENALQVVAKNV--AAF 312
QY 210 IGVDLEREGQVMTDNTPLQYNSNNEGEPSDPVGHEDCVEMLSGRWNTDECHLTMYF 269
Db 313 LSTMDSKTEGKTYPTGESLV-YSNWAPEFNDGGSDCVEIFTGKWDNACGEQRLV 371
QY 270 CEF 272
Db 372 CEF 374
RESULT 6
JN0450
conglutinin precursor - bovine
N:Alternate names: C3b-binding protein
N:Contains: conglutinin-N
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
A:Accession: JN0450; JC2396; S33235; A23740; S36879; S35044; I46010; A29416; S34054
R:Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A:Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
A:Reference number: JN0450; MUID:93213261; PMID:8460993
A:Accession: JN0450
A:Molecule type: mRNA
A:Residues: 1-371 <SUZ>
A:Cross-references: DDBJ:D14085; NID:9285643; PIDN:BA03170.1; PID:9285644
A:Experimental source: liver
R:Kawasaki, N.; Itoh, N.; Kawasaki, T.
Biochem. Biophys. Res. Commun. 198, 597-604, 1994
A:Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mammalian gene.
A:Reference number: JC2396; MUID:94128104; PMID:8297370
A:Accession: JC2396
A:Molecule type: mRNA
A:Residues: 1-371 <KAZ>
A:Note: The authors translated the codon GAT for residues 250 and 270 as Glu
R:Lu, J.; Laurson, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
Biochem. J. 292, 157-162, 1993
A:Title: The cDNA cloning of conglutinin and identification of liver as a primary site of
A:Reference number: S33235; MUID:93277452; PMID:7684896
A:Accession: S33235
A:Molecule type: mRNA
A:Residues: 1-172, 'H', 174-217, 'A', 219-271, 'V', 273-371 <LUJ>
A:Cross-references: EMBL:X71774; NID:9395267; PIDN:CAA50665.1; PID:9395268
A:Experimental source: liver
R:Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarna, T.B.
J. Biol. Chem. 266, 2715-2723, 1991
A:Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin family.
A:Reference number: A23740; MUID:91131556; PMID:1993651
A:Accession: A23740
A:Molecule type: protein
A:Residues: 21-209, 'S', 211-371 <LEB>
R:Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Biochem. Biophys. 305, 533-540, 1993
A:Title: Differentiation of conglutination activity and sugar-binding activity of conglutinin.
A:Reference number: S36879; MUID:93384312; PMID:8373191
A:Accession: S36879
A:Molecule type: protein
A:Residues: 21-54, 'S', 56-86, 'X', 88-89, 'X', 91, 'X', 93-94, 208-209, 'X', 211-227 <KAW>
A:Experimental source: serum
R:Lu, J.; Wiedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
Eur. J. Biochem. 215, 793-799, 1993
A:Title: Structural similarity between lung surfactant protein D and conglutinin. Two distinct
A:Reference number: S35044; MUID:93358905; PMID:8354286
A:Accession: S35044
A:Molecule type: protein
A:Residues: 75-86, 'X', 88-89, 'X', 91, 'I' <LUA>
A:Experimental source: lung
R:Young, N.M.; Leon, M.A.

A,Residues: 1-371 <LIO>
A,Cross-references: GB:U18871; NID:g495012; PIDN:AAA20126.1; PID:g495013
C:Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:248-369/Domain: C-type lectin homology <LCH>

Query Match 22.1%; Score 328.5; DB 2; Length 371;
Best Local Similarity 29.5%; Pred. No. 1e-19;
Matches 85; Conservative 35; Mismatches 95; Indels 73; Gaps 10;

46 PGRKGGDDGKGGP-----GEGKKGKVGRRGPKGIGKELGDMGRGNICK-----TGP 93
DB PGRKGGTGRGPGFMGPAGREGSGKQSGNPGFTPGPKGETGPKGGVGAPGIGQPPG 155
QY IGRKKGKGGKGLGIPGE-----KKGAG- 116
DB SGLKGEGKAGPETGAPGAGVTPGSGAIGPQPGSCARGPPGLKGDGRDGPGETGAKGESGL 215
QY TVCDGGRYKFGVQLDLSIARLKTSMKFKVKNVIAGIRETEKFKYIVQEE 166
DB AEYNALKQRVTILD-GHLRRFQN---AFSQYKKAIVLPDQGVG-----EKIFKTAGAV 265
QY KNYRESLTHCRIRGGMLAPKDEAAANTIADYVAKSGFFRFVIGVNDLREGQYMTDNT 226
DB KSYSDAEOLCREAKGGLASPRSSAENAVTQW-RAQEKNAVLSMNDISTEGRTYPTGE 324
QY PLONYSNWNEGP--SDPYGHEDCYEMLSGGWNTDCHLTWYFVCEFF 272
DB ILV-YSNWADGPNNSDGPQNCVIEIFPDGKWNVDVPCSKQLLVICFF 371

RESULT 8
LNRRBPS
pulmonary surfactant protein A precursor - rabbit
A,Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
A,Reference number: A29931; MUID:88139348; PMID:2830270
C:Accession: A29931
A,Accession: A29931
A,Molecule type: mRNA
A,Residues: 1-247 <BOG>
A,Cross-references: GB:J0542; NID:g165705; PIDN:AAA11465.1; PID:g165706
A,Note: 12-Pro was also found
A,Note: two species of mRNA, which appear to be transcribed from a single gene, could p
A,Note: the amino end of the mature protein is blocked
C:Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t
C:Comment: This protein is aialogycoprotein synthesized by alveolar type II cells. It
pendent on the presence of calcium ions
C:Superfamily: mannose-binding lectin; C-type lectin homology
C:Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glyco
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-247/Product: pulmonary surfactant protein A #status predicted <MAP>
F:27-99/Region: collagen-like
F:126-245/Domain: C-type lectin homology <LCH>
F:16/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F:206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.8%; Score 305.5; DB 1; Length 247;
Best Local Similarity 31.2%; Pred. No. 5.2e-18;
Matches 85; Conservative 30; Mismatches 104; Indels 53; Gaps 9;

25 SLGLIDISRTAEVCAHTHTI---SPQKDDGEGKDPGEKGKGVGRMGPKIGSLGD 81
DB SLALTLISAPSDCTDQVCIGSGPIGTPGSHLPGRDGRDGVKGDGPGGPMGPPGG 64
QY 82 M-----GDRGNIGHTGPIGKKDGKGLLIGIPEGKAGATVDCGRYKFKVGLD----- 132
DB 65 MPGLPGRDGLIGAPGVFGRGDKE-----PGERGPPG-----LPAYUDESLQA 108
QY 133 -----ISLARLKTSMKFKVKNVIAGIRETEKFKYIVQEEKNYRESLTHCRIRG 180

```
b 109 TLHLRHHLQSLGSLQSMKAV-----CEKIFSTNGQSVNPFDAIREVCARAG 158
y 181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQYNNWNEGEPS 240
b 159 GRIAVPRSLSENEAIAIVKERNY-AYLGLAEGTPAGFYLLDGDVPV-NYTNWYFGEP 216
y 241 DPYGHEDCVMLSGRWNDTECHLTWYFVCEP 272
b 217 G-QGREKCVENYTDGRWNDKNCLOQLVLCVCEP 247

RESULT 9
NR2WA
mannose-binding lectin A precursor - rat
;Alternate names: serum mannan-binding protein
;Species: Rattus norvegicus (Norway rat)
;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 22-Jun-1999
;Accession: B24791; A29556; A27799
;Dicikamer, K.; Dordal, M.S.; Reynolds, L.
;J. Biol. Chem. 261, 6878-6887, 1986
;Title: Mannose-binding proteins isolated from rat liver contain carbohydrate-recogniti
;otain.
;Reference number: A24791; MUID:86196130; PMID:3009480
;Accession: B24791
;Molecule type: mRNA
;Residues: 1-238 <DR1>
;Dicikamer, K.; McCreaty, V.
;J. Biol. Chem. 262, 2583-2589, 1987
;Title: Exon structure of a mannose-binding protein gene reflects its evolutionary rela
;Reference number: A29556; MUID:87137502; PMID:3029088
;Accession: A29556
;Molecule type: DNA
;Residues: 1-155, 'K', 157-238 <DR2>
;Cross-references: GB:M14104; GB:M14105; NID:9205259; PIDN:AAA98781.1; PID:9205261
;Note: The codon AAG for residue 156 is inconsistent with the authors' statement that b
;Ikeda, K.; Sanoh, T.; Kawasaki, N.; Kawasaki, T.; Yamashina, I.
;J. Biol. Chem. 262, 7451-7454, 1987
;Title: Serum lectin with known structure activates complement through the classical pa
;Reference number: A27799; MUID:87222358; PMID:3584121
;Accession: A27799
;Molecule type: protein
;Residues: 18-42 <IKE>
;Comment: Mannose-binding lectins are opsonins that are important in host defense again
;Keywords: acute phase; calcium; hydroxyllysine; hydroxyproline; lectin; liver; plasma
;1-17/Domain: signal sequence #status predicted <SIG>
;18-238/Product: mannose-binding lectin A #status experimental <MAT>
;36-88/Region: cell attachment
;85-87/Region: collagen-like
;118-234/Domain: C-type lectin homology <LCH>
;61,67,73/Modified site: 4-hydroxyproline (Pro) #status experimental
;79,82/Modified site: lysine derivative (Lys) (probably 5-hydroxylysine) #status experi

Query Match 19.5%; Score 290; DB 1; Length 238;
Best Local Similarity 28.7%; Pred. No. 9.6e-17;
Matches 75; Conservative 49; Mismatches 105; Indels 32; Gaps 8;

y 14 LLVFLFLQSLGLDLSRPTAEVCATHITSPGKGGDGPGEKGKGVGMGP 73
b 6 LLVLLCVSVSSGSGQ-TCETLTKTS--VIAGRDGRDGPGEKGEGQ-----GLR 55
y 74 GIKGELGDMGRNIGKTGPIGKKKGKGLLIGIPGEKGAGTVCDGCRVKKFFVGLDI 133
b 56 GLOGPPKGLGPPGSGVAPGSGQGPQGKGRG-----DSRAIEVLANMEA 100
y 134 SIARLKTSMKFNKNVIAGI--RETESKFFYIVQEEKNYRESLTHCRIRGGMAMPKDEAA 191
b 101 EINTLKSLELTNKLHAFSGKSGKGFVTHNRMPPFSKVALCSELRGTVAI PRNAEE 160
```

```
Qy 192 NTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQYNNWNEGEPSDPYGHEDCVEM 251
Db 161 NKAIQE-VAKTS---AFLGITDEVTEGQFMVYTGRL-TYSNWKKEDEPNDRSGSDCVTI 215
Qy 252 LSSGRWNDTECHLTWYFVCEP 272
Db 216 VDNGLWNDISCOASHTAUCEP 236

RESULT 10
LNMSMC
mannose-binding lectin C precursor - mouse
;Alternate names: Ra-reactive factor P28a
;Species: Mus musculus (House mouse)
;Date: 18-Jun-1993 #sequence revision 20-Feb-1998 #text_change 16-Jun-2000
;Accession: I48651; B46466; A42574; C42574
;R;Sastry, R.; Wang, J.S.; Brown, D.C.; Ezekowitz, R.A.; Tauber, A.I.; Sastry, K.N.
;Mamm. Genome 6, 103-110, 1995
;Title: Characterization of murine mannose-binding protein genes Mb11 and Mb12 reveals
;A;Reference number: I48650; MUID:95284466; PMID:7766991
;Accession: I48651
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-244 <SASI>
;Cross-references: EMBL:U09016; NID:G773286; PIDN:AAA82010.1; PID:G773288
;R;Sastry, K.; Zahedi, K.; Lelias, J.M.; Whitehead, A.S.; Ezekowitz, R.A.
;J. Immunol. 147, 692-697, 1991
;Title: Molecular characterization of the mouse mannose-binding proteins. The mannose-b
;A;Reference number: A46466; MUID:93302823; PMID:1712818
;Accession: B46466
;Molecule type: mRNA
;Residues: 1-2, 'L', 4-14, 'A', 16-244 <SAS2>
;Cross-references: GB:S42294; NID:G233017; PIDN:AAB19343.1; PID:G233018
;Experimental source: Inbred CBA/J, acute phase liver library, pTZ 19 vector
;Note: sequence extracted from NCBI backbone (NCBIN:42294, NCBI:42295)
;R;Kuge, S.; Ihara, S.; Watanabe, E.; Watanabe, M.; Takishima, K.; Suga, T.; Mamiya, G.;
;Biochemistry 31, 6943-6950, 1992
;Title: cDNAs and deduced amino acid sequences of subunits in the binding component of
;A;Reference number: A42574; MUID:92345256; PMID:1637828
;Accession: A42574
;Molecule type: mRNA; protein
;Residues: 1-244 <KUG>
;Cross-references: GB:D11440; NID:G220585; PIDN:BAA02005.1; PID:G220586
;Experimental source: BALB/c, liver
;Note: sequence extracted from NCBI backbone (NCBI:110137)
;Note: parts of the sequence, including the amino end of the mature protein, were confi
;Accession: C42574
;Molecule type: protein
;Residues: 19, 'X', 21-28, 'X', 30-32, 72-77, 'H', 79-80, 'G', 177-185; 187-189, 'H', 191-198 <KU2>
;Note: source is serum of ICR mice; differences may be allotypic
;Genetics:
;A;Gene: Mb12
;A;Introns: 59/1; 98/1; 121/1
;Superfamily: mannose-binding lectin; C-type lectin homology
;Keywords: calcium; endoplasmic reticulum; Golgi apparatus; homohexamer; hydroxyproline
;F;1-18/Domain: signal sequence #status predicted <SIG>
;F;19-244/Product: mannose-binding lectin C #status experimental <MAT>
;F;38-94/Region: collagen-like
;F;124-240/Domain: C-type lectin homology <LCH>
;F;29,34/Disulfide bonds: interchain #status predicted
;F;69/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 19.5%; Score 290; DB 1; Length 244;
Best Local Similarity 28.8%; Pred. No. 9.9e-17;
Matches 80; Conservative 56; Mismatches 100; Indels 42; Gaps 11;

Qy 1 MNGFASLLRNFILLVFLQLQISGLDIDSRPTAEVCATHITIS--PGPKGDDGEKGP 58
Db 1 MSPTFSFL-----LLCVTVVVAETLTGQVNSCPVVTCSPPGLNGFPKGRDGAKEK 55
Qy 59 GEEGKHGKGVGMGPXGIGELGDMGRNIGKTGPIGKKKGKGLLIGIPGEKGAGTV 118
```

```

Db 56 GBFGQ-----GLRGLQPPGKVGTPGPGNGLGKAVGPKGDRGDRA----- 97
QY 119 CDGCRYKFP-VQLDLSIARLTKSMKFKVN-VIAGISETEKEFYIVQBEKNVRESL-TH 175
Db 98 -----EFDISEIETALRSELRALRNWLSLSEKVGKKFYFVSSVKNSLDRVKAL 150
QY 176 CIRGMLAMPKDEAANTLIADYVAKSGFFRFVIGVNDLREGEQYMTDNTPIQ-NYSNW 234
Db 151 CSEFGQSVATPRNAENGAI-QKVAKD---IAYLGITDVRVEGS--FEDLTGNRVRYTNW 204
QY 235 NGEPSDPVGHEDCVEMLSGGWNDTECHLTWYFVCEP 272
Db 205 NDGEFNNTGDGDCVVLGNGKNDVPCSDSFLAICEF 242

RESULT 11
LNHUMC
mannose-binding lectin precursor [validated] - human
N:Alternate names: mannan-binding protein
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 08-Dec-2000
C:Accession: JLO115; S05641; A34978; JX0319; PC2188; A32266
R:Sastri, K.; Herman, G.A.; Day, L.; Deignan, E.; Bruns, G.; Morton, C.C.; Ezekowitz, R.
J. Exp. Med. 170, 1175-1189, 1989
A:Title: The human mannose-binding protein gene. Exon structure reveals its evolutionary
A:Reference number: JLO115; MUID:90010778; PMID:2477486
A:Accession: JLO115
A:Molecule type: DNA
A:Residues: 1-248 <SAS>
A:CROSS-references: EMBL:X15422; NID:G34486; PIDN:CAA33462.1; PID:G34487
R:Taylor, M.B.; Brickell, P.M.; Craig, R.K.; Summerfield, J.A.
Biochem. J. 262, 763-771, 1989
A:Title: Structure and evolutionary origin of the gene encoding a human serum mannose-bi
A:Reference number: S05641; MUID:90073571; PMID:2590164
A:Accession: S05641
A:Molecule type: DNA
A:Residues: 1-248 <TAY>
A:CROSS-references: EMBL:X15954; NID:G34480; PIDN:CAA34079.1; PID:G1212951
A:Accession: A34978
A:Molecule type: protein
A:Residues: 'X', 22-24, 'X', 26, 'X', 28-31, 'X', 33-34, 'X', 36, 'XXXX', 41-50 <TAY2>
R:Szekowicz, R.A.B.; Day, L.E.; Herman, G.A.
J. Exp. Med. 167, 1034-1046, 1988
A:Title: A human mannose-binding protein is an acute-phase reactant that shares sequence
A:Reference number: JLO027; MUID:86171281; PMID:2450948
A:Accession: JLO027
A:Molecule type: mRNA
A:Residues: 1-2, 'C', 4, 'IT', 8, 'S', 10-57, 'R', 59-60, 'GT', 63-106, 'PCLRLK', 113, 'SSANRNGTYQ', 1
R:Kurata, H.; Samon, T.; Kozutsuami, Y.; Yokota, Y.; Kawasaki, I.
J. Biochem. 115, 1148-1154, 1994
A:Title: Structure and function of mannan-binding proteins isolated from human liver and
A:Reference number: JX0319; MUID:95073978; PMID:7982896
A:Accession: JX0319
A:Molecule type: protein
A:Residues: 1-248 <KURI>
A:Accession: PC2188
A:Molecule type: mRNA
A:Residues: 1-20 <KUR2>
A:Experimental source: liver and serum
C:Comment: Mannose-binding lectins are opsonins that are important in host defense again
C:Comment: This protein is a Ca2+-requiring animal lectin specific for mannose and N-acet
C:Genetics:
A:Gene: GDB:MBL
A:CROSS-references: GDB:120167; OMIM:154545
A:Map position: 10q11.2-10q11.2
A:Introns: 63/1; 102/1; 125/1
C:Superfamily: mannose-binding lectin; C-type lectin homology
C:Keywords: acute phase; calcium binding; endoplasmic reticulum; Golgi apparatus; hydrox
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-248/Product: mannose-binding lectin #status experimental <MAT>
F:42-99/Region: collagen-like
F:128-244/Domain: C-type lectin homology <LCH>
F:47,73,79,82,88/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

```

```

Query Match 19.5%; Score 289.5; DB 1; Length 248;
Best Local Similarity 31.1%; Pred. No. 1.1e-16;
Matches 75; Conservative 37; Mismatches 100; Indels 29; Gaps 7;

QY 34 PTAVCAHTHIS--PGPKGDDGKGPGGEGKKGKVGMPGKIGKELGMDGDRNGIKT 91
Db 33 PAVIACSPGTINGPPGKDGDRGDTKGKGEFGQ-----GLRGLQPPGKLGPPGPGPS 85
QY 92 GPICKKDGKGGKLLGIPGKKGKAGTVCDCGRYRKFGVGLDLSIARLTKSMKFKVNVIAG 151
Db 86 GSPGPKGKGKGGP-----KSPDGSSLSAASERK---ALQTEMARIKWLTFSLG---- 131
QY 152 IRETEKFFYIVQBEKNYRESLTHCRIRGGLMLAMPDEAANTLIADYVAKSGFFRFVIGV 211
Db 132 -KQVGNKFFLTNGEIMTFEKVKALCVKQFQSVATPRNAENGAIQNLKE-----EAFLG 186
QY 212 NDLEREGQYMTDNTPIQNYSNNEGEPSPDYGHEDCVEMLSGGWNDTECHLTWYFVCE 271
Db 187 TDETEGQFVLTGNRL-TYTNWNEGEPNAGSDEDCVLLKNGQWNDVPCSTSHLAVCE 245
QY 272 F 272
Db 246 F 246

RESULT 12
LNHUPI
pulmonary surfactant protein A precursor (clone 1A) - human
N:Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: B25720
R:Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.
J. Biol. Chem. 261, 9029-9033, 1986
A:Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfact
A:Reference number: A25720; MUID:86250832; PMID:3755136
A:Accession: B25720
A:Molecule type: mRNA
A:Residues: 1-248 <FLO>
A:CROSS-references: GB:K03475
A:Note: part of the sequence was confirmed by protein sequencing
A:Note: the amino end of the mature protein, which was not identified, is partially ace
A:Note: clones corresponding to two different proteins were sequenced. Cotranslational
C:Genetics:
A:Gene: GDB:SFTPL1; SP-A; SP-A1
A:CROSS-references: GDB:119593; OMIM:178630
A:Map position: 10q22-10q23
C:Superfamily: mannose-binding lectin; C-type lectin homology
C:Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glyco
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F:127-246/Domain: C-type lectin homology <LCH>
F:21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted
F:30,33,36,42,54,57,63,76,79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status pre
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.3%; Score 287; DB 1; Length 248;
Best Local Similarity 28.2%; Pred. No. 1.8e-16;
Matches 75; Conservative 44; Mismatches 117; Indels 30; Gaps 9;

QY 14 ILLVLFILQISGLD:DSRPTAEVCAHTTISPQKGDGKGPCEGKGKVGKVGMPK 73
Db 6 LALTLLIIMASGAACEV-----KDVCGV---SPGIFGTGSHGLPDRDGLKGDGPP 57
QY 74 GIKGELGDM-----GDRGNIGKTGPIGKKGDKGKGLGIPGEXKAGTVCDCGRYRKFGV 129
Db 58 GPMGPPGETPCPGNNGLPGAPGVGEKGEKGE-----PGERGPPGLPAHLDE----- 105
QY 130 QLDLSIARLTKSMKFKVNVI---GIRETEKFFYIVQBEKNYRESLTHCRIRGGLMLAMP 186
Db 106 ELQATLHDFRQILQITRGALSQSGSMTVGEKVFSSNGOSITFDATQACARAGGIAPV 165

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Y 187 KDBAANTLIADYVAKSGPRFVIGVNDLREGQYMTDNTPLQYNNWNEGSPDPYCHE 246
b 166 RNPENEAASFKKNTY-AVGLTEGSPGDFRYSDDTGV-NYTNWYRGEPAAG-RGKE 222
Y 247 DCEVEMSSGRWNTDCHLTMVFCF 272
b 223 QCVEMYTDQWDRNCLYSRLTICF 248
RESULT 13
NUP6
pulmonary surfactant protein A precursor (genomic clone) - human
N;Alternate names: alveolar proteinosis protein; pulmonary surfactant 32K apoprotein; pu
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: A24622; A3628
White, R.T.; Damm, D.; Miller, J.; Spratt, K.; Schilling, J.; Hawgood, S.; Benson, B.
ature 317, 361-363, 1985
Title: Isolation and characterization of the human pulmonary surfactant apoprotein ge
Reference number: A24622; MUID:86014366; PMID:2995821
Accession: A24622
Molecule type: DNA
Residues: 1-248 <WHI>
Cross-references: GB:M30838; NID:g190564; PIDN:AAA36510.1; PID:g190565
Note: The sequence in GenBank entry HUMPSAP, release 109.0, (PID:g190565) has the cod
Note: four nucleotide differences, producing amino acid differences at positions 45, 5
Haagsman, H.P.; White, R.T.; Schilling, J.; Lau, K.; Benson, B.J.; Golden, J.; Hawgood
m. J. Physiol. 257, L421-L429, 1989
Title: Studies of the structure of lung surfactant protein SP-A.
Reference number: A43628; MUID:90119861; PMID:2610270
Accession: A43628
Molecule type: protein
Residues: 143-150/220-240/243-248 <HAA>
Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t
Comment: This protein is a sialoglycoprotein synthesized by alveolar type II cells. It
end on the presence of calcium ions.
Genetics:
Gene: GDB:SFTPA1; SFTP1; SP-A; SP-A1
Cross-references: GDB:119593; OMIM:178630
Map position: 10q22-10q23
Introns: 58/1; 98/1; 124/1
Superfamily: mannose-binding lectin; C-type lectin homology
Keywords: alveolar proteinosis; calcium; gaseous exchange; glycoprotein; hydroxylsine
1-20/Domain: signal sequence #status predicted <SIG>
21-248/Product: pulmonary surfactant protein A #status predicted <NAF>
28-100/Domain: collagenous #status predicted <COL>
127-246/Domain: C-type lectin homology <LCH>
30,33,36,42,57,63,76,79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status predict
51,88/Modified site: 5-hydroxylsine (Lys) #status predicted
155-246,224-238/Disulfide bonds: #status experimental
207/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 19.2%; Score 285.5; DB 1; Length 248;
Best Local Similarity 30.6%; Pred. No. 2.4e-16;
Matches 74; Conservative 37; Mismatches 112; Indels 19; Gaps 8;
Y 38 VCATHI---SPGKDDKDEKDPGEKHKVGMGPKGKGLGDMG-DRGNIGTKGP 93
b 19 VCVKDVGVSGPIPTPGSHGLGRHGRDGLGDLGPPGMPGPGPCPPGNDGLPGA 78
Y 94 IGKKGDKGKGLGIPGEGKAGTCDCCORVKKFVQGLDLSIARLKTSMKFKVNVIA-- 150
b 79 PGIPGCGEK--GEBGEGPPGLPAHLDE-----ELQATLHDFRHIQTRGALSQ 129
Y 151 GIRETEKFFYIVQEKVNSLTHCRTRGGMLAMPKDEAANTLIADYVAKSGPRFVIG 210
b 130 SIMTVGKVFSSNGQSITPDAIQEACARAGRIAPRNPENEAASFKKNTY-AVGL 188
Y 211 VNDLREGQYMTDNTPLQYNNWNEGSPDPYGHEDCVEMSSGRWNTDCHLTMVFC 270
b 189 LTEGSPGDFRYSDDTGV-NYTNWYRGEPAAG-RGKEQCVEMYTDQWDRNCLYSRLTIC 246

QY 271 EF 272
Db 247 EF 248

RESULT 14

IS1921

pulmonary surfactant-associated protein A1 - human

N;Alternate names: SP-A1

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999

C;Accession: IS1921

R;Katyal, S.L.; Singh, G.; Locker, J.

Am. J. Respir. Cell Mol. Biol. 6, 446-452, 1992

A;Title: Characterization of a second human pulmonary surfactant-associated protein SP-A

A;Reference number: IS1921; MUID:92198680; PMID:1372511

A;Accession: IS1921

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-248 <RES>

A;Cross-references: GB:M88519; NID:g338048; PIDN:AAA60319.1; PID:g338049

C;Genetics:

A;Gene: GDB:SFTPA1; SFTP1; SP-A; SP-A1

A;Cross-references: GDB:119593; OMIM:178630

A;Map position: 10q22-10q23

A;Introns: 58/1; 98/1; 124/1

C;Superfamily: mannose-binding lectin; C-type lectin homology

F;127-246/Domain: C-type lectin homology <LCH>

Query Match 19.2%; Score 284.5; DB 2; Length 248;

Best Local Similarity 31.2%; Pred. No. 2.9e-16;

Matches 70; Conservative 37; Mismatches 110; Indels 7; Gaps 5;

QY 53 GBKGDPEGKHKVGMGPKGKGLGDMGDRGNIGTKG-PICKKDGKGLGIPGE 111

Db 28 GSPGIPGPGSHGLPGRDGRGVKGPDPGPPGPGTETPCPPNNGLPGAPGVPGERGE 87

QY 112 KKAQTVDCORVKKFVQGLDISIARLKTSMKFKVNVIA--GIRETEKFFYIVQEK 168

Db 88 KGEAGERPPGLPAHLDEELQATLHDFRHIQTRGALSQGSIMTVGKVFSSNGQSIT 147

QY 169 YRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPRFVIGVNDLREGQYMTDNTPL 228

Db 148 FDAIQEACARAGRIAPRNPENEAASFKKNTY-AVGLTEGSPGDFRYSDDTGV 206

QY 229 QNYSNNWNEGSPDPYGHEDCVEMSSGRWNTDCHLTMVFCF 272

Db 207 -NYTNWYRGEPAAG-RGKEQCVEMYTDQWDRNCLYSRLTICDF 248

RESULT 15

LNUP6

pulmonary surfactant protein A precursor (clone 6A) - human

N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999

C;Accession: A25720

R;Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;

J. Biol. Chem. 261, 9029-9033, 1986

A;Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfacta

A;Reference number: A25720; MUID:86250832; PMID:3755136

A;Accession: A25720

A;Molecule type: mRNA

A;Residues: 1-248 <FLO>

A;Cross-references: GB:M3686; NID:g190669; PIDN:AAA60211.1; PID:g190670

A;Note: part of the sequence was confirmed by protein sequencing

A;Note: the amino end of the mature protein, which was not identified, is partially acet

A;Note: clones corresponding to two different proteins were sequenced. Cotranslational m

C;Genetics:

A;Gene: GDB:SFTPA1; SFTP1; SP-A; SP-A1

A;Cross-references: GDB:119593; OMIM:178630

A;Map position: 10q22-10q23

C;Superfamily: mannose-binding lectin; C-type lectin homology

C:Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glycd
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F:127-246/Domain: C-type lectin homolog <LCH>
F:21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted
F:30,33,36,42,54,57,63,76,79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status pred
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 284; DB 1; Length 248;
Best Local Similarity 29.9%; Pred. No. 3.2e-16;
Matches 78; Conservative 42; Mismatches 119; Indels 22; Gaps 9;

QY 16 LVFLLIQIQLDIDSDRPTAEVCATHTISPPKXGDDGKGPGEKGKGVGRMGPKGI 75
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 6 LALNLILMAASGAACEVK---DVCVG---SPGIPGSHGLPGDGRDGLKGDGPPGP 59
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 76 KGEIGDMG-DRGNIGKTPIGKKGDKGKGLLIPGKKGAGTVCDGCRYKRVGQLDIS 134
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 60 MGPPGEMPCPPGNDGLGAPGIPGCGEK--GPFGERGPPGLPAHLDE-----ELQAT 110
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 135 IARLKTSMKFFVKNVIA--GIRETEEKFYIVQBEKNYRESLTHCRIRGGMLAMPKDEAA 191
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 111 LHDFRHQILQTRGALSLOGSINTVCEKVFSSNGQSITFDALQECACAGGRIAVPRNPEE 170
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 192 NTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQNYSNWNEGSPDPYGHEDCEVM 251
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 171 NEAIAAFVKKYNNTY-AYVGLTEGSPSGDFRYSGDGTPV-NYTNWYRGEPAG-RGKEQCQVEM 227
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 252 LSSGRWNTDECHLTWYVCEP 272
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 228 YTDGQWDRNCLYSLITICEP 248
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

Search completed: February 24, 2004, 02:25:01
Job time : 29 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: February 24, 2004, 02:22:42 ; Search time 23 Seconds
(without alignments)
621.756 Million cell updates/sec

file: US-09-600-932-2
effect score: 1484
equences: 1 MNGFASLLRRNQFILLVFLP.....NDTECHLTMYFVCFIKKK 277

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Gapop 10.0 , Gapext 0.5

searched: 389414 seqs, 51625971 residues

total number of hits satisfying chosen parameters: 389414

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/prodata/2/1aa/5B COMB.pap.*
- 3: /cgn2_6/prodata/2/1aa/6A COMB.pap.*
- 4: /cgn2_6/prodata/2/1aa/6B COMB.pap.*
- 5: /cgn2_6/prodata/2/1aa/PCTUS COMB.pap.*
- 6: /cgn2_6/prodata/2/1aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	328.5	22.1	351	3	US-09-011-735-1
2	328.5	22.1	351	4	US-09-029-156-1
3	289.5	19.5	248	4	US-09-198-603C-2
4	205	13.8	519	4	US-09-453-702B-265
5	202.5	13.6	128	4	US-09-535-521-8
6	202.5	13.6	139	4	US-09-535-521-11
7	202.5	13.6	141	4	US-09-535-521-14
8	202.5	13.6	187	4	US-09-535-521-17
9	202.5	13.6	208	4	US-09-535-521-20
10	202.5	13.6	292	4	US-09-535-521-2
11	202.5	13.6	292	4	US-09-535-521-5
12	201	13.5	123	4	US-09-535-521-25
13	191.5	12.9	1024	3	US-08-931-820-2
14	191.5	12.9	1366	3	US-08-963-825-19
15	191.5	12.9	1366	4	US-09-500-811-19
16	191.5	12.9	1366	4	US-09-570-573-19
17	191.5	12.9	1366	4	US-09-548-608-19
18	191.5	12.9	1366	4	US-09-585-887-10
19	191.5	12.9	1366	4	US-09-289-578-10
20	187.5	12.6	489	2	US-08-794-795-7
21	187.5	12.6	489	3	US-09-249-200-7
22	187.5	12.6	492	3	US-08-468-996-11
23	187.5	12.6	518	1	US-08-392-367B-2
24	187.5	12.6	518	3	US-08-893-467A-2
25	187	12.6	161	3	US-09-011-735-6
26	184.5	12.4	399	4	US-09-134-000C-6019
27	184.5	12.4	404	4	US-09-517-603-2

28	181.5	12.2	128	4	US-09-227-357-190	Sequence 130, App
29	180	12.1	107	6	5514562-17	Patent No. 5514582
30	180	12.1	557	3	US-09-320-095-10	Sequence 10, Appl
31	180	12.1	557	3	US-09-523-487-10	Sequence 10, Appl
32	179	12.1	495	2	US-08-794-795-2	Sequence 2, Appl
33	179	12.1	495	3	US-09-249-200-2	Sequence 2, Appl
34	179	12.1	520	2	US-08-794-795-6	Sequence 6, Appl
35	179	12.1	520	3	US-09-249-200-6	Sequence 6, Appl
36	178	12.0	285	4	US-09-312-283C-182	Sequence 382, App
37	177.5	12.0	1017	4	US-08-468-996-10	Sequence 10, Appl
38	177.5	12.0	1060	3	US-08-931-820-3	Sequence 3, Appl
39	177.5	12.0	1418	3	US-08-963-825-20	Sequence 20, Appl
40	177.5	12.0	1418	3	US-09-010-999-1	Sequence 1, Appl
41	177.5	12.0	1418	4	US-09-500-811-20	Sequence 20, Appl
42	177.5	12.0	1418	4	US-09-570-573-20	Sequence 20, Appl
43	177.5	12.0	1418	4	US-08-548-608-20	Sequence 20, Appl
44	177	11.9	294	3	US-09-188-930-294	Sequence 294, App
45	177	11.9	294	4	US-09-312-283C-294	Sequence 294, App

ALIGNMENTS

RESULT 1
US-09-011-735-1
; Sequence 1, Application US/09011735B
; Patent No. 6110708
; GENERAL INFORMATION:
; APPLICANT: Wakamiva, No. 6110708utaka
; TITLE OF INVENTION: Recombinant Conglutinin and Producing Method Thereof
; FILE REFERENCE: 19036/34548
; CURRENT APPLICATION NUMBER: US/09/011.735B
; CURRENT FILING DATE: 1998-05-22
; EARLIER APPLICATION NUMBER: JP 7-209698
; EARLIER FILING DATE: 1995-08-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Bovine
US-09-011-735-1

Query Match	22.1%;	Score 328.5;	DB 3;	Length 351;
Best Local Similarity	29.2%;	Pred. No. 6.9e-25;		
Matches	84;	Conservative	33;	Mismatches 98; Indels 73; Gaps 9;
QY	46	PGPKGDGEGKDP-----GEGKHGKVGVRMPGPKGIGELGMDGRNICK-----TGP	93	
Db	76	PGPKGDTGPRGPPGMPGPGAGREGPSGKSGSGPPGTPGPKGTGPKGVGAPGQGGPPG	135	
QY	94	IGKKGDKGKGLLGIPEKKGAG-----	116	
Db	136	SLGKGEKAPGETGAPGAGVTGPGSAGIPGPGSGARPPGLKGDRODPOGTGASGSL	195	
QY	117	-----TVCDGGRYKFKVQGLDISIAELKTSMKFVNVIAGIRETEKPYIVQEE	166	
Db	196	AFVNALKRVTILD-GHLRRFQN-----AFSQKAVLPDQAVG-----EKIETAGAV	245	
QY	167	KNYRESLTHCIRGMLAMPKDEAANTLIADYVAKSFFRVFIGNDLREGQVMFTDNT	226	
Db	246	KSYDAEOLCREAKQLASPRSSAENAVTQWV-RAQEKAYLSMNDISTEGRTYPTGE	304	
QY	227	PLQYNNNEGEP--SDPYGHEDCVMLSSGRWNTDCHLTMYFVCEP	272	
Db	305	ILV-YSNWADGEPPNSDEGPENCVEIFPDGKNWDPVPCSKOLLIVICEP	351	

RESULT 2
US-09-029-156-1
; Sequence 1, Application US/09029156
; Patent No. 6365342
; GENERAL INFORMATION:

APPLICANT: WAKAMIYA, No. 6365342utaka
TITLE OF INVENTION: RECOMBINANT CONGLUTININ AND PRODUCING
TITLE OF INVENTION: METHOD THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/029,156
FILING DATE: 02-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00173
FILING DATE: 02-OCT-1995
APPLICATION NUMBER: PCT/JP95/02035
FILING DATE: 02-OCT-1995
APPLICATION DATA:
APPLICATION NUMBER: JPA - 209698
FILING DATE: 17-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gasa, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 19036/34546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-029-156-1

Query Match 22.1%; Score 328.5; DB 4; Length 351;
Best Local Similarity 29.2%; Pred. No. 6.9e-25;
Matches 84; Conservative 33; Mismatches 98; Indels 73; Gaps 9;
QY 46 PGPKGDDGKGDG-----GEGKHGKVGKGMGPKGKIGELGDMGDRGNIGK-----TGP 93
DB 76 PGPKGDTGPRGPGMPGPGAGREGSGKQSGMGPPGTPGPKGTGPKGGVGAQIQGPPGP 135
QY 94 IGKKGDKGKGLGIPGKKGAG-----116
DB 136 SGLKGEKAGPGETGAPGAGVTGPGSAGIGPQPSGARGPPGLKGRDGPGETGASGESGL 195
QY 117 -----TVCDGGRYKRVGQLDISIAELKTSMAFVKNVIAIGIRETEEPYIVQEE 166
DB 196 AEVNAKQKVILD-GHLRRQN-----AFSQYKAVLPDQAVG-----EKIFKTAGAV 245
QY 167 KNYRESLTHCIRGNLAMPDEAANTLIADYVAKSGFFRVFGVNDLREGQYMTDNT 226
DB 246 KSYDAEQLCREAKGQLASPRSSAENAVTQMV-RAQEKNAIYLSMNDISTEGRTYFTGE 304
QY 227 PLQNSYNNNEGP--SDPYGHEDCVEMLSGRWNTDCHLTMTYFVCEF 272
DB 305 ILV-YSNWADGEPNNSDEQPCNVCVEIFPDGKNDVPCSKQLLVICF 351

RESULT 3
US-09-198-603C-2
; Sequence 2, Application US/09198603C
; Patent No. 6337193

GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; FILE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198,603C
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human
US-09-198-603C-2
Query Match 19.5%; Score 289.5; DB 4; Length 248;
Best Local Similarity 31.1%; Pred. No. 3.6e-21;
Matches 75; Conservative 37; Mismatches 100; Indels 29; Gaps 7;
QY 34 PTAEVCAHTHIS--PGPKGDDGKGDGPGEGKHGKVGKGMGPKGKIGELGDMGDRGNIGK 91
DB 33 PAVIACSSPGINGFPGRDGRDGTGKGEKGPQ-----GLRGLQPPGKLGPPGPGPS 85
QY 92 GPIGKKDKGKGLGIPGKKGKAGTVCDCGRYKRVGQLDISIAELKTSMAFVKNVIAIG 151
DB 86 GSPGPKGQKGDG-----KSPDGDSLSAASERK---ALQTEMARIKKWLTFSLG---- 131
QY 152 IRETEEKFYIVQEEKNYRESLTHCIRGNLAMPDEAANTLIADYVAKSGFFRVFGV 211
DB 132 -KQVGNKFFLTNGEIMTFEKKVKALCVKFOASVATPNAEAENGAIONLIKE-----BAFLGI 186
QY 212 NDLEREGQYMTDNTPLQNSYNNNEGPSPDPYGHEDCVEMLSGRWNTDCHLTMTYFVCE 271
DB 187 TDEKTEGQFVDLAGNRL-TYTNWNEGEPNNSAGSDRDCVLLKNGQWNVPCSTSHLAVCE 245
QY 272 F 272
DB 246 F 246
RESULT 4
US-09-453-702B-265
; Sequence 265, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955

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; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 11
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-11

Query Match      13.6%; Score 202.5; DB 4; Length 139;
Best Local Similarity 37.6%; Pred. No. 9.4e-13;
Matches 44; Conservative 21; Mismatches 47; Indels 5; Gaps 3

QY 156 BEKFYIVQEEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLE 215
DB 22 QKQCYFGEPEKKWIQARFACKLQGLASIHSGEEQDFLARYANKKG---TWIGLRDLD 78

QY 216 RGQYMTDNTPLQYNSWNNEGSPDPYGHEDCVEMLSSGRWNDETECHLTM-YFVCE 271
DB 79 REGEFIWMDENPL-NYSNWRPGEPNNGQGQEDCYMMQSGQWDAFCGSSLDGWVCD 134

RESULT 7
US-09-535-521-14
; Sequence 14, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 14
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-14

Query Match      13.6%; Score 202.5; DB 4; Length 141;
Best Local Similarity 37.6%; Pred. No. 9.6e-13;
Matches 44; Conservative 21; Mismatches 47; Indels 5; Gaps 3

QY 156 BEKFYIVQEEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLE 215
DB 24 QKQCYFGEPEKKWIQARFACKLQGLASIHSGEEQDFLARYANKKG---TWIGLRDLD 80

QY 216 RGQYMTDNTPLQYNSWNNEGSPDPYGHEDCVEMLSSGRWNDETECHLTM-YFVCE 271
DB 81 REGEFIWMDENPL-NYSNWRPGEPNNGQGQEDCYMMQSGQWDAFCGSSLDGWVCD 136

RESULT 8
US-09-535-521-17
; Sequence 17, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5

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; CURRENT APPLICATION NUMBER: US/09/535,521
; EARLIER FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-17

Query Match 13.6%; Score 202.5; DB 4; Length 187;

Best Local Similarity 37.6%; Pred. No. 1.4e-12;
Matches 44; Conservative 21; Mismatches 47; Indels 5; Gaps 3;
QY 156 BEKYYIVQEEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLE 215
Db 70 QKCYFGEPEPKWQAFACSKLQGRLASIHSQEQDFLARYANKG---TWIGLRDLD 126
QY 216 REGQYMTDNTPLQYNNWNEGSPDPYGHEDCVEMLSGRWNTDECHLTW-YFVCE 271
Db 127 REGEFIWMDENPL-NYSNWRPGEPPNGGQEDCVMMQSGQWMDAFCGSSLDGWCD 182

RESULT 9

US-09-535-521-20
; Sequence 20, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; EARLIER FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-20

Query Match 13.6%; Score 202.5; DB 4; Length 208;

Best Local Similarity 37.6%; Pred. No. 1.6e-12;
Matches 44; Conservative 21; Mismatches 47; Indels 5; Gaps 3;
QY 156 BEKYYIVQEEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLE 215
Db 91 QKCYFGEPEPKWQAFACSKLQGRLASIHSQEQDFLARYANKG---TWIGLRDLD 147
QY 216 REGQYMTDNTPLQYNNWNEGSPDPYGHEDCVEMLSGRWNTDECHLTW-YFVCE 271
Db 148 REGEFIWMDENPL-NYSNWRPGEPPNGGQEDCVMMQSGQWMDAFCGSSLDGWCD 203

RESULT 10

US-09-535-521-2
; Sequence 2, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; EARLIER FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913

; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-2

Query Match 13.6%; Score 202.5; DB 4; Length 292;

Best Local Similarity 37.6%; Pred. No. 2.6e-12;
Matches 44; Conservative 21; Mismatches 47; Indels 5; Gaps 3;
QY 156 BEKYYIVQEEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLE 215
Db 175 QKCYFGEPEPKWQAFACSKLQGRLASIHSQEQDFLARYANKG---TWIGLRDLD 231
QY 216 REGQYMTDNTPLQYNNWNEGSPDPYGHEDCVEMLSGRWNTDECHLTW-YFVCE 271
Db 232 REGEFIWMDENPL-NYSNWRPGEPPNGGQEDCVMMQSGQWMDAFCGSSLDGWCD 287

RESULT 11

US-09-535-521-5
; Sequence 5, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-5

Query Match 13.6%; Score 202.5; DB 4; Length 292;

Best Local Similarity 37.6%; Pred. No. 2.6e-12;
Matches 44; Conservative 21; Mismatches 47; Indels 5; Gaps 3;
QY 156 BEKYYIVQEEKYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLE 215
Db 175 QKCYFGEPEPKWQAFACSKLQGRLASIHSQEQDFLARYANKG---TWIGLRDLD 231
QY 216 REGQYMTDNTPLQYNNWNEGSPDPYGHEDCVEMLSGRWNTDECHLTW-YFVCE 271
Db 232 REGEFIWMDENPL-NYSNWRPGEPPNGGQEDCVMMQSGQWMDAFCGSSLDGWCD 287

RESULT 12

US-09-535-521-25
; Sequence 25, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1


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; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500.811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: collagen alpha 2- type I
;
US-09-500-811-19

Query Match          12.9%; Score 191.5; DB 4; Length 1366;
Best Local Similarity 43.5%; Pred. No. 2.7e-10;
Matches 40; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 46 PGPKGDDGKGDPEEGKHGKVGKMGPKIGKELGDMGDRGNIGTKTGPIGKK----- 97
Db 558 PGPSPGAGEVGVKPGKGRGLHGEFGLPGPAGPRGERGPPGSGAGAGTGPICGRGFSGPPGP 617
QY 98 -GDKGKGLL-----GIPGEXKGAG 116
Db 618 DGNKGEPGVGVGAVGTAGSPGSLPGERGAAG 649

Search completed: February 24, 2004, 02:29:32
Job time : 24 secs
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result No.	Score	Query #		Length	DB	ID	Description
		Match	%				
1	1472	99.2	277	9	US-09-978-325A-97		Sequence 97, Appl
2	1472	99.2	277	9	US-09-978-337-97		Sequence 97, Appl
3	1472	99.2	277	9	US-09-978-192A-97		Sequence 97, Appl
4	1472	99.2	277	9	US-09-999-832A-97		Sequence 97, Appl
5	1472	99.2	277	10	US-09-978-189-97		Sequence 97, Appl
6	1472	99.2	277	10	US-09-978-608A-97		Sequence 97, Appl
7	1472	99.2	277	10	US-09-978-585A-97		Sequence 97, Appl
8	1472	99.2	277	10	US-09-978-191A-97		Sequence 97, Appl
9	1472	99.2	277	10	US-09-978-403A-97		Sequence 97, Appl
10	1472	99.2	277	10	US-09-978-564A-97		Sequence 97, Appl
11	1472	99.2	277	10	US-09-999-833A-97		Sequence 97, Appl
12	1472	99.2	277	10	US-09-981-915A-97		Sequence 97, Appl
13	1472	99.2	277	10	US-09-978-824-97		Sequence 97, Appl
14	1472	99.2	277	10	US-09-918-585A-97		Sequence 97, Appl
15	1472	99.2	277	10	US-09-978-423A-97		Sequence 97, Appl

PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 9; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
y 1 MNGFASLLRNQFILLVLFLLQISLGLDIDSRPTAEVCATHTISPGKGGDGEKGPGE 60
b 1 MNGFASLLRNQFILLVLFLLQISLGLDIDSRPTAEVCATHTISPGKGGDGEKGPGE 60
y 61 EKGKGVGMGPKIGKELGMDGRGNICKTGPICKKDGKKGKLLGIPGKKGAGTVCD 120
b 61 EKGKGVGMGPKIGKELGMDGQGNIGKTGPICKKDGKKGKLLGIPGKKGAGTVCD 120
y 121 CGRYKRVQQLDISARLKTSMKFKVNVIAIGIRETEEFKYIVQEEKNYRESLTHCRIRG 180
b 121 CGRYKRVQQLDISARLKTSMKFKVNVIAIGIRETEEFKYIVQEEKNYRESLTHCRIRG 180
y 181 GMLAMPKDEAANTLADYVAKSGFFRVFGVNDLREGEQYMTDNTPLQYSNWNEGEPS 240
b 181 GMLAMPKDEAANTLADYVAKSGFFRVFGVNDLREGEQYMTDNTPLQYSNWNEGEPS 240
y 241 DYPGHEDCVEMLSGRWNTDECHLTMYFVCFIKKK 277
b 241 DYPGHEDCVEMLSGRWNTDECHLTMYFVCFIKKK 277

ESULT 2
S-09-978-697-97
Sequence 97, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070

APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Rapiet, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 9; Length 277;
Best Local Similarity 99.3%; Pred No. 1, 4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNGFASLRNFILLVFLIQISGLDIDSRPTAECVATHITSPGKDDGKDPGE 60
QY 61 EGKHGVGMGPKGKGELGDMGRNIGKTGPICKGDKGKGLGIPGKKGAGTVCD 120
DB 61 EGKHGVGMGPKGKGELGDMGRNIGKTGPICKGDKGKGLGIPGKKGAGTVCD 120
QY 121 CGYRKFFVQQLDISIARLKTSMKFKVNIAGIRETEEFYIVQEEKYRESLTHCRIRG 180
DB 121 CGYRKFFVQQLDISIARLKTSMKFKVNIAGIRETEEFYIVQEEKYRESLTHCRIRG 180
QY 181 GMLMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQYMTDNTPLQYNNWNEGPS 240
DB 181 GMLMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQYMTDNTPLQYNNWNEGPS 240
QY 241 DPYGHEDCVEMLSGRWNTDECHLTWYFVCFIFKXK 277
DB 241 DPYGHEDCVEMLSGRWNTDECHLTWYFVCFIFKXK 277

RESULT 4
US-09-999-832A-97

; Sequence 97, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deshoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US/09/999, 832A
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; D_g 9; Length 277;

Best Local Similarity 99.3%; Pred. No. 1.4e-137; Mismatches 1; Indels 0; Gaps 0;
Matches 275; Conservative

QY 1 MNGFASLLRRNQFILLVFLFIQISLGLDIDSRPTAEVCATHITISPGKGDGKGPGE 60
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DB 61 EKHGKVGVMGPKIGKELGDMGDRGNIGKTGPIGKKGDKGKGLLIGPKGKAGTVCD 120
QY 121 CGYRKFGVQLDISIARLKTSMKFKVKNVIAGIRTEKFFYVVOEEKNYRESLTHCRIRG 180
DB 121 CGYRKFGVQLDISIARLKTSMKFKVKNVIAGIRTEKFFYVVOEEKNYRESLTHCRIRG 180
QY 181 GMLAMPKDEAAANTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQYSNWNEGPS 240
DB 181 GMLAMPKDEAAANTLIADYVAKSGFFRVFIGVNDLREGQYMTDNTPLQYSNWNEGPS 240
QY 241 DPYGHEDCVMELSSGRWNTDTECHLTMTFVCEFIKXKX 277
DB 241 DPYGHEDCVMELSSGRWNTDTECHLTMTFVCEFIKXKX 277

RESULT 5

US-09-978-189-97

/ Sequence 97, Application US/09978189
/ Publication No. US20030004102A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630PIC7
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/ CURRENT FILING DATE: 2001-10-15
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PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Y 1 MNGFASLLRRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEGKDPGE 60
b 1 MNGFASLLRRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEGKDPGE 60
Y 61 EGKHGKVRGPKGKGEKGLDMDGRNIGKTPGIGKKGDKGKGLLGPGEKAGTVCD 120
b 61 EGKHGKVRGPKGKGEKGLDMDGQDNIGKTPGIGKKGDKGKGLLGPGEKAGTVCD 120
Y 121 CGRYRKFVQGLDISIARLKTSMKFNKVIAGIRETEEFYIVQEKYRSLTHCRIRG 180
b 121 CGRYRKFVQGLDISIARLKTSMKFNKVIAGIRETEEFYIVQEKYRSLTHCRIRG 180
Y 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQYMTDNTPLQNSNNWNEGEP 240

Db 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQYMTDNTPLQNSNNWNEGEP 240
Qy 241 DPGHEDCVEMLLSSGRWNTDTECHLTMYFVCFIKKK 277
Db 241 DPGHEDCVEMLLSSGRWNTDTECHLTMYFVCFIKKK 277

RESULT 6

US-09-978-608A-97
; Sequence 97, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-97

Query Match 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MNGFASLLRRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEGKDPGE 60
Db 1 MNGFASLLRRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEGKDPGE 60
Qy 61 EGKHGKVRGPKGKGEKGLDMDGRNIGKTPGIGKKGDKGKGLLGPGEKAGTVCD 120
Db 61 EGKHGKVRGPKGKGEKGLDMDGQDNIGKTPGIGKKGDKGKGLLGPGEKAGTVCD 120
Qy 121 CGRYRKFVQGLDISIARLKTSMKFNKVIAGIRETEEFYIVQEKYRSLTHCRIRG 180
Db 121 CGRYRKFVQGLDISIARLKTSMKFNKVIAGIRETEEFYIVQEKYRSLTHCRIRG 180
Qy 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQYMTDNTPLQNSNNWNEGEP 240
Db 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQYMTDNTPLQNSNNWNEGEP 240
Qy 241 DPGHEDCVEMLLSSGRWNTDTECHLTMYFVCFIKKK 277

Db 241 DPYGHEDCVEMLSGRWNDTECHLTWYFVCFIKKKK 277

RESULT 7
US-09-978-585A-97

Sequence 97, Application US/09978585A
Publication No. US20030049633A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 97
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGFASLLRNQFILLVFLIQISGLDIDSRPTAEVCATHTISPGKGDGKGPGE 60
DB 1 MNGFASLLRNQFILLVFLIQISGLDIDSRPTAEVCATHTISPGKGDGKGPGE 60
QY 61 EKGHKGVMGPKGKIGELGMDGRNIGKTGPIGKKGDKGKGLGIPGKKGAGTVCD 120
DB 61 EKGHKGVMGPKGKIGELGMDGMDQGNIGKTGPIGKKGDKGKGLGIPGKKGAGTVCD 120
QY 121 CGRYKRVFVQGLDITSLARKTSMKFKVNIAGIRETEEFYIVQEEKYRESLTHCRIG 180
DB 121 CGRYKRVFVQGLDITSLARKTSMKFKVNIAGIRETEEFYIVQEEKYRESLTHCRIG 180
QY 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVNDLEREGQYMTDNTPLQYNNNEGEPS 240
DB 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNVNDLEREGQYMTDNTPLQYNNNEGEPS 240
QY 241 DPYGHEDCVEMLSGRWNDTECHLTWYFVCFIKKKK 277
DB 241 DPYGHEDCVEMLSGRWNDTECHLTWYFVCFIKKKK 277

RESULT 8

US-09-978-191A-97
Sequence 37, Application US/09978191A
Publication No. US20030050239A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
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PRIOR APPLICATION NUMBER: 60/081952
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PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query March 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNGFASLLRRNQFILLVLFLLQISGLDIDSRPTAEVCATHTSPGPKGDDGKGDPE 60
Db 1 MNGFASLLRRNQFILLVLFLLQISGLDIDSRPTAEVCATHTSPGPKGDDGKGDPE 60
Qy 61 EGKHGKVGKMGPKGKIGKGLGMDGRNIGKTGPIGKKGDKGKGLLGPGEKKGAGTYCD 120
Db 61 EGKHGKVGKMGPKGKIGKGLGMDGDCNIGKTGPIGKKGDKGKGLLGPGEKKGAGTYCD 120
Qy 121 CGRYKFKVGQLDISIAKLKTSKMKFVNVIAGIRETEEFYIVQEKYRESLTHCRIRG 180
Db 121 CGRYKFKVGQLDISIAKLKTSKMKFVNVIAGIRETEEFYIVQEKYRESLTHCRIRG 180

QY 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQVFTDNTPLQYNNWNEGEPS 240
DB 181 GMLAMPKDEAANTLIADYVAKSGFRFVIGVNDLREGQVFTDNTPLQYNNWNEGEPS 240
QY 241 DPYGHDCVEMSSGRWNTDTECHLTMTYFVCEFIKXKX 277
DB 241 DPYGHDCVEMSSGRWNTDTECHLTMTYFVCEFIKXKX 277

RESULT 9

US-09-978-403A-97
Sequence 97, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
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PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796

PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
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PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
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PRIOR APPLICATION NUMBER: 60/083742
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PRIOR APPLICATION NUMBER: 60/084441
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
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PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 MNGFASLLRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGKGPGE 60
|||||

Db 1 MNGFASLLRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGKGPGE 60
Qy 61 EKGKGKVGWGPKGIGKGLGDMGDGNGIKTGPIGKKGDKGKGLIGTPGKKGAGTVC 120
Db 61 EKGKGKVGWGPKGIGKGLGDMGDGNGIKTGPIGKKGDKGKGLIGTPGKKGAGTVC 120
Qy 121 CGYRKRFVQGLDISIARLKTSMKPKVKNVIAGIRETEEXFYIVQEEKYRSLTHCRIRG 180
Db 121 CGYRKRFVQGLDISIARLKTSMKPKVKNVIAGIRETEEXFYIVQEEKYRSLTHCRIRG 180
Qy 181 GMLAMPKDEAANTLIADYVAKSGPFRFVGNDLREBQYMTDNTPLQNTSYNNNEGEP 240
Db 181 GMLAMPKDEAANTLIADYVAKSGPFRFVGNDLREBQYMTDNTPLQNTSYNNNEGEP 240
Qy 241 DPYGHEDCVEMLSGRWMDTECHLTMYFVCFEIKKK 277
Db 241 DPYGHEDCVEMLSGRWMDTECHLTMYFVCFEIKKK 277
RESULT 10
US-09-978-564A-97
; Sequence 97, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

PRIOR APPLICATION NUMBER:	60/082704
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082804
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082700
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082796
PRIOR FILING DATE:	1998-04-23
PRIOR APPLICATION NUMBER:	60/083336
PRIOR FILING DATE:	1998-04-27
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083392
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083495
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083496
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083499
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083545
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083554
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083742
PRIOR FILING DATE:	1998-04-30
PRIOR APPLICATION NUMBER:	60/084366
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084414
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084441
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084637
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084639
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084598
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085339
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085338
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085323
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085689
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085579
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085580
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085573
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085704

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MNGFASLLRRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGKGDPE 60
b 1 MNGFASLLRRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGKGDPE 60

61 EGKHGKVGVRGPKIGKEIGELMDGRNIGKTPGPKGDKGKGLLGPGEKAGTVC 120
b 61 EGKHGKVGVRGPKIGKEIGELMDGRNIGKTPGPKGDKGKGLLGPGEKAGTVC 120

121 CGYRKRVGGLDLSIARLKTSMKFPVKNVIAGIRETEKEFYIIVQBEKNYRESLTHCRIRG 180
b 121 CGYRKRVGGLDLSIARLKTSMKFPVKNVIAGIRETEKEFYIIVQBEKNYRESLTHCRIRG 180

181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMTDNTPLQYNSNWNNEGEPS 240
b 181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMTDNTPLQYNSNWNNEGEPS 240

241 DPYGHEDCVEMLSGRWNTDTECHLTWYFVCEFTKXKX 277
b 241 DPYGHEDCVEMLSGRWNTDTECHLTWYFVCEFTKXKX 277

RESULT 11
JS-09-999-833A-97
Sequence 97, Application US/09999833A
Publication No. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertszen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James,
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P26301C65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
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;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query March 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFLLQIQSLGLDIDSRPTAEVCATHTISPPGKDDGEXGDFGE 60
DB 1 MNGFASLLRRNQFILLVFLFLLQIQSLGLDIDSRPTAEVCATHTISPPGKDDGEXGDFGE 60

QY 61 EGKKGKVGKRGPKGIKGELODMGRNIGKTGPIGKKGDKGKGLLIGPEKKGAGTVC 120
DB 61 EGKKGKVGKRGPKGIKGELODMGRNIGKTGPIGKKGDKGKGLLIGPEKKGAGTVC 120

QY 121 CGYRKKEVQGLDISIARLKTSMKFKVKNVIAGIRETEKEKFFYIVQEEKNYRESLTHCRIRG 180
DB 121 CGYRKKEVQGLDISIARLKTSMKFKVKNVIAGIRETEKEKFFYIVQEEKNYRESLTHCRIRG 180

QY 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNDLREGQYMTDNTPLQNYNNWNEGEPS 240
DB 181 GMLAMPKDEAANTLIADYVAKSGFFRVFVGNDLREGQYMTDNTPLQNYNNWNEGEPS 240

QY 241 DPYGHEDCVELSSGRWNTDECHLTWYFVCEPIKXXX 277
DB 241 DPYGHEDCVELSSGRWNTDECHLTWYFVCEPIKXXX 277

RESULT 12
US-09-981-915A-97
; Sequence 97, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981.915A

[illegible][illegible]

;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred No. 1,4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGFASILLRNQFILLVFLLIQISGLDIDSRPTAEVCAHTTISPGKGDGKDPGE 60
DB 1 MNGFASILLRNQFILLVFLLIQISGLDIDSRPTAEVCAHTTISPGKGDGKDPGE 60
QY 61 EGHGKGVGWSGPKGKGELGMDGDSNGTKGTGKKGKGLLGIPEGKKGAGTVCD 120
DB 61 EGHGKGVGWSGPKGKGELGMDGDSNGTKGTGKKGKGLLGIPEGKKGAGTVCD 120
QY 121 CGRYKRVGQGLDISIARLKTSMKFKVNIAGIRETEEFYIVQEKYRESLTHCRIRG 180
DB 121 CGRYKRVGQGLDISIARLKTSMKFKVNIAGIRETEEFYIVQEKYRESLTHCRIRG 180
QY 181 GMLAMPKDEAANTLADYVAKSGFRVFTGVNDLREGEQYMTDNTPLQYNNWNEGPS 240
DB 181 GMLAMPKDEAANTLADYVAKSGFRVFTGVNDLREGEQYMTDNTPLQYNNWNEGPS 240
QY 241 DPYGHEDCVEMLSGGWNDTECHLTYVFCFIKKK 277
DB 241 DPYGHEDCVEMLSGGWNDTECHLTYVFCFIKKK 277

RESULT 13
US-09-978-824-97
;; Sequence 97, Application US/09978824
;; Publication No. US20030055216A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann

;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C14
;; CURRENT APPLICATION NUMBER: US/09/978,824
;; CURRENT FILING DATE: 2001-10-17
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
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;; PRIOR APPLICATION NUMBER: 60/077791
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;; PRIOR APPLICATION NUMBER: 60/078004
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 10; Length 277;
Best Local Similarity 99.3%; Pred. No. 1.4e-137;
Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLQLQSLGLDIDSDPTAEVCATHIISPPKGGDDGKDPGE 60
DB 1 MNGFASLLRRNQFILLVFLQLQSLGLDIDSDPTAEVCATHIISPPKGGDDGKDPGE 60
QY 61 EGKHKVGRMGPKGKIGELGDMGDRGNIGTKTGPIGKKGKGLLGIPEEKAGTVC 120
DB 61 EGKHKVGRMGPKGKIGELGDMGDRGNIGTKTGPIGKKGKGLLGIPEEKAGTVC 120
QY 121 GRYRKFVQGLDISIARKTSMKFKVKNVIAGIRETEKFFYIVQEEKVNEESLTHCRIG 180
DB 121 GRYRKFVQGLDISIARKTSMKFKVKNVIAGIRETEKFFYIVQEEKVNEESLTHCRIG 180
QY 181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMFDTNTPLOYSNNNEGPS 240
DB 181 GMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMFDTNTPLOYSNNNEGPS 240
QY 241 DPYGHDCVEMLSGRWNTDTECHLTMYFVCEFTKXKX 277
DB 241 DPYGHDCVEMLSGRWNTDTECHLTMYFVCEFTKXKX 277

RESULT 14
US-09-918-585A-97
; Sequence 97, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Par, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023

Query Match 99.2%; Score 1472; DB 10; Length 277;

Best Local Similarity 99.3%; Pred. No. 1.4e-137;

Matches 275; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2y 1 MNGFASLLRNQFLLVFLLOQSLGLDSDRPTAEVCATHTISPGKGDGEGDPE 60
db 1 MNGFASLLRNQFLLVFLLOQSLGLDSDRPTAEVCATHTISPGKGDGEGDPE 60
2y 61 EGKRGKVRMGFKIGELGDMGDRGNIGKTGPIGKKGDKGKGLLGIPEKRGKAGTVCD 120
db 61 EGKRGKVRMGFKIGELGDMGDRGNIGKTGPIGKKGDKGKGLLGIPEKRGKAGTVCD 120
2y 121 CGYRKFGVQLDISIARKTSMKFKVKNVIAGIRETEKFPYIVOREKNYRESLTHCRING 180
db 121 CGYRKFGVQLDISIARKTSMKFKVKNVIAGIRETEKFPYIVOREKNYRESLTHCRING 180
2y 181 GMLAMPKDEAANTLIADYVAKSGFFRFVIGVNDLREGQVMTDNTPLQYNSWNNEGEPS 240
db 181 GMLAMPKDEAANTLIADYVAKSGFFRFVIGVNDLREGQVMTDNTPLQYNSWNNEGEPS 240
2y 241 DPYGHEDCVEMLSGRWNDETECHLTMTYFVCEFTKXKK 277
db 241 DPYGHEDCVEMLSGRWNDETECHLTMTYFVCEFTKXKK 277

RESULT 15

US-09-978-423A-97

; Sequence 97, Application US/09978423A

; Publication No. US20030069178A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.2%; Score 1472; DB 10; Length 277;

Best Local Similarity 99.3%; Pred. No. 1.4e-137; Indels 0; Gaps 0;
Matches 275; Conservative 1; Mismatches 1;

QY 1 MNGFASLLRRNQFILLVLLQIQLSLGLDIDSRPTAEVCATHTISPGPKDDGKDPGE 60
DB 1 MNGFASLLRRNQFILLVLLQIQLSLGLDIDSRPTAEVCATHTISPGPKDDGKDPGE 60
QY 61 EKHGKVGVMGPKGIKGBELGDMGRNIGTKPIGKDKGKGLLGIPEGKKGAGTVCD 120
DB 61 EKHGKVGVMGPKGIKGBELGDMGRNIGTKPIGKDKGKGLLGIPEGKKGAGTVCD 120
QY 121 CGYRKRFVQGLDISIARLKTSMKFVNVIAGIRETEBKFFYIVQEEKNYRESLTHCSIRG 180
DB 121 CGYRKRFVQGLDISIARLKTSMKFVNVIAGIRETEBKFFYIVQEEKNYRESLTHCSIRG 180
QY 181 GMLAMPKDEANTLIADYVAKSGFRFVIGVNDLEREQYMTDNTPLQYSNWNEGEPS 240
DB 181 GMLAMPKDEANTLIADYVAKSGFRFVIGVNDLEREQYMTDNTPLQYSNWNEGEPS 240
QY 241 DPYGHEDCVEMLSGRWNTDECHLTMYFVCFIKKK 277
DB 241 DPYGHEDCVEMLSGRWNTDECHLTMYFVCFIKKK 277

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M nucleic - nucleic search, using sw model

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(without alignments)
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Maximum Match 100%

Listing first 45 summaries

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- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
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- 7: gb.pl.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.ba.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.man.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1141.6	71.6	182475	2	AC023487	AC023487 Homo sapi
5	980.2	61.5	1016	6	AX376032	AX376032 Sequence
6	980.2	61.5	1016	9	AY359038	AY359038 Homo sapi
7	655.8	41.1	867	10	AB016429	AB016429 Mus muscu
8	358.2	22.5	496	6	AX410041	AX410041 Sequence
9	344.4	21.6	166900	2	AC115924	AC115924 Mus muscu
10	344.4	21.6	223510	2	AC123656	AC123656 Mus muscu
11	344.4	21.6	345420	2	AC131337	AC131337 Mus muscu
12	343	21.5	234922	2	AC097055	AC097055 Rattus no
13	268.2	16.8	1272	5	BC056052	BC056052 Xenopus 1
14	246	15.4	1238	6	AR252616	AR252616 Sequence
15	246	15.4	1238	6	AX403469	AX403469 Sequence
16	246	15.4	1238	6	AX454582	AX454582 Sequence
17	246	15.4	1238	6	AX491060	AX491060 Sequence
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21	244.6	15.3	813	6	BD103332	BD103332 Novel col
22	240.6	15.1	1522	6	BD103307	BD103307 Novel col
23	239	15.0	813	6	BD103338	BD103338 Novel col
24	235.2	14.7	1139	6	BD103303	BD103303 Novel col
25	233.8	14.7	735	6	BD103333	BD103333 Novel col
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27	211	13.2	1417	9	BC009951	BC009951 Homo sapi
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37	189.4	11.9	995	6	BD103304	BD103304 Novel col
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ALIGNMENTS

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E29008

LOCUS

E29008

DEFINITION

Novel collectin.

ACCESSION

E29008

VERSION

E29008.1 GI:13018416

KEYWORDS

JP 1999206377-A/1.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1595)

AUTHORS

Nobutaka, W.

TITLE

Novel collectin

JOURNAL

Patent: JP 1999206377-A 1 03-AUG-1999;

1595 bp DNA linear PAT 18-JUN-2001

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COMMENT
FUSO YAKUHIN KOGYO KK
CS Homo sapiens (human)
PN JP 1999206377-A/1
PD 03-AUG-1999
PF 23-JAN-1998 JP 1998011281
PR
PI NOBUTAKA WAKAMIYA
PC C12N15/09, C07K14/47, C07K14/78, C12P21/00, C12N15/00 CC
Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 6..836.
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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DB 1 CAGCAATGAATGGCTTGCATCTCTGGTTCGAGAAACCAATTATCCCTCGTACTAT 60
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DB 121 GTGCCACACACACAATTTCCAGGAGCCCAAGAGATGATGTGAAAAAGGAGATCCAG 180
QY 181 GAGAGAGGGAAGCATCGCAAGCTGGAGCCGATGGGCGGAAAGGAATTAAGGAGAAC 240
DB 181 GAGAGAGGGAAGCATCGCAAGCTGGAGCCGATGGGCGGAAAGGAATTAAGGAGAAC 240
QY 241 TGGGTGATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 300
DB 241 TGGGTGATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 300
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RESULT 2
AB002631
LOCUS Homo sapiens mRNA for collectin 34, complete cds.
DEFINITION Homo sapiens mRNA for collectin 34, complete cds.
ACCESSION AB002631
VERSION AB002631.1 GI:5162874
KEYWORDS collectin 34.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
AUTHORS Ohtani, K., Suzuki, Y., Eda, S., Kawai, T., Kase, T., Yamazaki, H.,
Keshi, H., Sakai, Y., Fukuh, A., Sakamoto, T. and Wakamiya, N.

```

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Ohtani, K.
TITLE
JOURNAL
Direct Submission
Submitted (04-APR-1997) Katsuki Ohtani, Osaka Prefectural Institute
of Public Health, Department of Pathology; 3-69, Nakamichi 1-chome
Higashinari-ku, Osaka, Osaka 537, Japan
(E-mail:suzuk@iph.pref.osaka.jp, Tel:+81-6-972-1321,
Fax:+81-6-972-0772)
FEATURES
Location/Qualifiers
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YIVGEKNRESLTCIRLGNLAMPDDEAANTLIADYVAKSGFPRVFIGVNDLERG
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K"
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RIGIN
Query Match 99.9%; Score 1594; DB 9; Length 1594;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 CAGCAATGAATGCTTTGCATCCTTGTCTCGAAGAACCAATTTATCTCTCTGTACTAT 60
b 1 CAGCAATGAATGCTTTGCATCCTTGTCTCGAAGAACCAATTTATCTCTCTGTACTAT 60
Y 61 TTCTTTTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTACCGCTGAACTCT 120
b 61 TTCTTTTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTACCGCTGAACTCT 120
Y 121 GTGCCACACACAAATTTCCACAGACCCCAAGGAGATGATGGTCAAAAAGGAGATCCAG 180
b 121 GTGCCACACACAAATTTCCACAGACCCCAAGGAGATGATGGTCAAAAAGGAGATCCAG 180
Y 181 GAGAGAGGGAAGCATGTCGCAAGTGGACGCGATGGGGCCGAAAGGAATTAAGGAGAAC 240
b 181 GAGAGAGGGAAGCATGTCGCAAGTGGACGCGATGGGGCCGAAAGGAATTAAGGAGAAC 240
Y 241 TGGGTGATATGGAGATCGGGCAATATTGGCAAGCTGGGCCCATTTGGGAAGAGGGTG 300
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b 361 GTGATTTGGAGATACCGGAAATTTTGTGGCAACTGGATATTAGTATTCGCCGGTCA 420
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RESULT 3
AC080033

LOCUS

AC080033 141262 bp DNA linear PRI 20-FEB-2002
 Homo sapiens chromosome 8, clone RP11-885J16, complete sequence.

ACCESSION

AC080033

VERSION

AC080033.10 GI:18767530

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 141262)

AUTHORS

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE

Homo sapiens chromosome 8, clone RP11-885J16

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 141262)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,
 Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
 DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
 FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
 Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
 Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
 McPeeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
 O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
 Pierre,N., Pisan,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
 Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
 Sounez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Tirrell,A., Travers,M., Triglio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zimmer,A. and Zody,M.

Direct Submission

TITLE

Submitted (23-SEP-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL

3 (bases 1 to 141262)

REFERENCE

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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 Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
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 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosatti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE

Submitted (15-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL

4 (bases 1 to 141262)

REFERENCE

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
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 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE

Submitted (20-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL

On Feb 20, 2002 this sequence version replaced gi:18653568.

COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L10939

Center clone name: 895_J_16

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repeat_region	/rpt_family="L1ME1"	56415	TTGATCTGAGTCAACATAGCTAGAAAATGCTAACTGAGGTATGGAGCCTCCATCATCAT	56474
repeat_region	9899..10022			
repeat_region	/rpt_family="L1PB3"	987	GCTCTTTTGTGATGATTTTCATATTTTTCACATGCTATGTTTATGACCCCAATACTCGC	1046
repeat_region	10245..10649			
repeat_region	/rpt_family="HAL1"	56475	GCTCTTTTGTGATGATTTTCATATTTTTCACATGCTATGTTTATGACCCCAATACTCGC	56534
repeat_region	10921..12580			
repeat_region	/rpt_family="HAL1"	1047	CAGGTTACATGGGTCTTGAGAGAGAAATTTAACTAACTTGTGACAGAGATAGTTGGTT	1106
repeat_region	complement(12616..12915)			
repeat_region	/rpt_family="AluSx"	56535	CAGGTTACATGGGTCTTGAGAGAGAAATTTAACTAACTTGTGACAGAGATAGTTGGTT	56594
repeat_region	complement(13402..13869)			
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repeat_region	complement(14079..14128)			
repeat_region	/rpt_family="L3"	56595	GTCCTATATGTCAAATGAGTTGTTCTCTGTTGTTTGTCTCTGTTGTTTGTCTCTCTCTCT	56654
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repeat_region	/rpt_family="AT rich"	1167	TCGTGTCTATCCAGTGGATTAATTTCCAGTTTACTGCTGATGATGATGATGATGATGATG	1226
repeat_region	complement(14623..14738)			
repeat_region	/rpt_family="MIR3"	56655	TCGTGTCTATCCAGTGGATTAATTTCCAGTTTACTGCTGATGATGATGATGATGATGATG	56714
repeat_region	14892..15130			
repeat_region	/rpt_family="MIR"	1227	ATGTTTAGGCTAACCTGCGCTGCGCCCAAGCCAGACATGTACAAGGGCTTTCTGTGACCA	1286
repeat_region	15183..15254			
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repeat_region	/rpt_family="MER1A"	1287	ATGATAAGATCTTTGAATCCAAGATGCCAGATGTTTACCAGTCCACACCTATGGCCAT	1346
repeat_region	15711..16021			
repeat_region	/rpt_family="AluSx"	56775	ATGATAAGATCTTTGAATCCAAGATGCCAGATCTTTTACCAGTCCACACCTATGGCCAT	56834
unsure	15784..15788			
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Best Local Similarity	99.7%; Pred. No. 8.5e-280;			
Matches 1144; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
2Y	447 GTGATAGCAGGATAGGGAACCTGAGAGAAATTTCTACTACATCGTGCAGAGAGAG	506		
Db	55935 GTGATAGCAGGATAGGGAACCTGAGAGAAATTTCTACTACATCGTGCAGAGAGAG	55994		
2Y	507 AACTACAGGGAATCCCTAACCCACTCAGGATTCGGGGTGGAAATGCTAGCCATGCCCAAG	566		
Db	55995 AACTACAGGGAATCCCTAACCCACTCAGGATTCGGGGTGGAAATGCTAGCCATGCCCAAG	56054		
2Y	567 GATGAAGCTCCACACACTCATCGTACTATGTTGCCAAGAGTGGCTTCTTTGGGGTG	626		
Db	56055 GATGAAGCTCCACACACTCATCGTACTATGTTGCCAAGAGTGGCTTCTTTGGGGTG	56114		
2Y	627 TTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTACATGTTTCAGACAACACTCCA	686		

RESULT 4

AC023487/C

LOCUS

DEFINITION

ACCESSION

AC023487 182475 bp DNA linear HTG 26-MAR-2001.
Homo sapiens chromosome 8 clone RP11-164H21, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
AC023487

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AC023487.10 GI:13357236
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 182475)
Abola A.P., Bruno D., Conn L., Della Rosa M., Faulkner D.,
Federspiel N., Glukhov S., Hansen N., Herman Z.S., Hyma R.,
Mao J., Komp C., Kottler S., Lam B., Marathe R., Miranda M.,
Morehouse A.J., Nguyen M., Oefner P., Palm C.J., Ramirez D.,
Southwick A.M., Webb C., Wilhelmy J., Yu S. and Davis R.W.
Unpublished
2 (bases 1 to 182475)
Bruno D., Conn L., Della Rosa M., Faulkner D., Federspiel N.,
Glukhov S., Hansen N., Hyma R., Mao J., Marathe R.,
Morehouse A.J., Oefner P., Palm C.J., Ramirez D., Wilhelmy J.,
Yu S. and Davis R.W.
Direct Submission
Submitted (14-FEB-2000) DNA Sequencing and Technology Center.
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
On Mar 16, 2001 this sequence version replaced gi:13324778.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SPSDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: 844
Center clone name: RP11-164H21
----- Summary Statistics
Sequencing Vector: M13mp18; X02513; 98% of reads
Chemistry: Dye-terminator; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180260 bases at least Q40
Consensus quality: 180441 bases at least Q30
Consensus quality: 180507 bases at least Q20
Insert size: 178614; agarose-fp
Insert size: 182275; sum-of-contigs
Quality coverage: 8.1x in Q20 bases; agarose-fp
Quality coverage: 7.9x in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 42072: contig of 42072 bp in length
* 42073 42172: gap of unknown length
* 42173 109254: contig of 67082 bp in length
* 109255 109354: gap of unknown length
* 109355 182475: contig of 73121 bp in length.
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ORIGIN
Query Match      71.6%; Score 1141.6; DB 2; Length 182475;
Best Local Similarity 99.7%; Pred. No. 8.4e-280;
Matches 1144; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 447 GTGATACAGGGATTAGGAACTGAAGAGAAATTTCTACTATCATCGTCAGGAAGAGAG 506
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QY 507 AACTACAGGGAATCCCTAACCCACTCGAGATTCGGGGTGGATGCTAGCCATGCCAAG 566
Db 6173 AACTACAGGGAATCCCTAACCCACTCGAGATTCGGGGTGGATGCTAGCCATGCCAAG 6114
QY 567 GATGAAGCTCCCAACACATCATCGCTGACTATGTTGCCAAGAGTGGCTTTCTCGGGTG 626
Db 6113 GATGAAGCTCCCAACACATCATCGCTGACTATGTTGCCAAGAGTGGCTTTCTCGGGTG 6054
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QY 687 CTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGGACCCCTTATGTCATGAGGAC 746
Db 5993 CTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGGACCCCTTATGTCATGAGGAC 5934
QY 747 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACAGAGTGCCATCTTACCATTGATAC 806
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QY 807 TTTCTGTGTGAGTTTCATCAAGAAGAAAAGTAACTTCCCTCATCTCTACGATTTGCTATT 866
Db 5873 TTTCTGTGTGAGTTTCATCAAGAAGAAAAGTAACTTCCCTCATCTCTACGATTTGCTATT 5814
QY 867 TTCTGTGACGGTCATTACAGTTATGTTTATCCATCTCTTTTCTCTGATTGCTACAT 926
Db 5813 TTCTGTGACGGTCATTACAGTTATGTTTATCCATCTCTTTTCTCTGATTGCTACAT 5754
QY 927 TTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGTATGAGGACCTCCATCATCAT 986
Db 5753 TTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGTATGAGGACCTCCATCATCAT 5694
QY 987 GCTCTTTTGTGATGATTTTTCATATTTTTCACACATGTTGTTATGACCCCAATACTCCG 1046
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Db 5513 TCTGTGCTATCCCAAGTGGATAATTTCCCAAGTTTACTTGGTGATGATTAGGAAGTTGTTG 5454
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QY 1287 ATGATAAGATCTTTGAATCCAGATGCCAGATGTTTACCAGTCACACCCCTATGGCCAT 1346
Db 5393 ATGATAAGATCTTTGAATCCAGATGCCAGATGTTTACCAGTCACACCCCTATGGCCAT 5334
QY 1347 GGCTATACCTGGAAAGTTCTCTCTTGTGGCACAGACATAGAAATGCTTTTAAACCCCAAGCCT 1406
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Query Match      61.5%; Score 980.2; DB 9; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.2e-238;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB      77 TTCCTTTGCAAAATCAGAGTCTGGGTCTGGATATGATAGCCGTCCTACCGCTGAAGTCT 136
QY      121 GTGCCACACACACAAATTTCCACAGAGACCCAAAGAGATGATGGTGAAAAAGGAGATCCAG 180
DB      137 GTGCCACACACACAAATTTCCACAGAGACCCAAAGAGATGATGGTGAAAAAGGAGATCCAG 196
QY      181 GAGAGAGGAAAGCATGGCAAGTGGACGCGATGGGCCGCAAAAGGAATTAAGAGAGAAC 240
DB      197 GAGAGAGGAAAGCATGGCAAGTGGACGCGATGGGCCGCAAAAGGAATTAAGAGAGAAC 256
QY      241 TGGGTGATATGGAGATCGGGCATATATGGCAAGATCGGCCCATTTGGGAAGAGGGTG 300
DB      257 TGGGTGATATGGAGATCAGGCAATATATGGCAAGATCGGGCCCATTTGGGAAGAGGGTG 316
QY      301 ACAAGGGGAAAAAGTTTGTCTTGAATACCTGGAGAAAAAGCAAGCAGTACTGTCT 360
DB      317 ACAAGGGGAAAAAGTTTGTCTTGAATACCTGGAGAAAAAGCAAGCAGTACTGTCT 376
QY      361 GTGATTGTGAAGATACCGGAATTTGTGACAACTGGATATTAGTATTGCCCGGCTCA 420
DB      377 GTGATTGTGAAGATACCGGAATTTGTGACAACTGGATATTAGTATTGCCCGGCTCA 436
QY      421 AGACATCTATGAAGTTTGTCAAGATGTGATAGCAGGGAATTAGGGAACCTGAAGAGAAAT 480
DB      437 AGACATCTATGAAGTTTGTCAAGATGTGATAGCAGGGAATTAGGGAACCTGAAGAGAAAT 496
QY      481 TCTACTACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC 540
DB      497 TCTACTACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC 556
QY      541 GGGGTGGAATGCTTAGCCATGCCCAAGGATGAAGCTGCCCAACACACTCATCGCTGACTATG 600
DB      557 GGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCCAACACACTCATCGCTGACTATG 616
QY      601 TTGCCAAGAGTGGCTTCTTTTGGGTGTTCAATTGGCGTGAATGACCTTGAAGAGGAGGAC 660
DB      617 TTGCCAAGAGTGGCTTCTTTTGGGTGTTCAATTGGCGTGAATGACCTTGAAGAGGAGGAC 676
QY      661 AGTACATGTTCCACAGACACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 720
DB      677 AGTACATGTTCCACAGACACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 736
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QY      721 CCAGCGAGCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCAGATGAATG 780
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QY      781 ACACAGAGTGCCTATCTTACCATGATCTTTGTCTGTGTGAGTTTCATCAAGAAAGAAAAAGTAAAC 840
DB      797 ACACAGAGTGCCTATCTTACCATGATCTTTGTCTGTGTGAGTTTCATCAAGAAAGAAAAAGTAAAC 856
QY      841 TTCCCTCATCTAGTAGTATTGCTGATTTTCTGTGACCGTCATACAGTTATTGTTATCCA 900
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QY      901 TCCCTTTTCTGATTTACTACTACATTTGATCTGAGTCAACATAGCTAGAAATGCTAAA 960
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DB      977 CTGAGGTATGGAGCTCCATCATCA 1001

RESULT 7
AB016429
LOCUS      Mus musculus mRNA for collectin-L1, complete cds.
DEFINITION
ACCESSION AB016429
VERSION    AB016429.1 GI:27530340
KEYWORDS   collectin-L1.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
            Kawai,T., Suzuki,Y., Eda,S., Kase,T., Ohtani,K., Sakai,Y.,
            Keshi,H., Fukuhara,A., Sakamoto,T., Nozaki,M., Copeland,N.G.,
            Jenkins,N.A. and Wakamiya,N.
            Molecular cloning of mouse collectin liver 1
            Biosci. Biotechnol. Biochem. 66 (10), 2134-2145 (2002)
22333927
12450124
MEDLINE
PUBMED
REFERENCE   2 (bases 1 to 867)
            Kawai,T. and Suzuki,Y.
            Direct Submission
            Submitted (21-JUL-1998) Takao Kawai, Osaka Prefectural Institute of
            Public Health, Laboratory of Food Microbiology, 3-69 Nakamichi
            1-chome, Higashinari-ku, Osaka 537-0025, Japan
            (E-mail:kawai@iph.pref.osaka.jp, Tel:81-6-972-1321,
            Fax:81-6-972-2393)
            Location/Qualifiers
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                YIVVEKNYRESLTHCRIGMLAMPXDEAANTLIADYVAKSGFFRVFIVGNLREB
                QYMS"TDNTPLQNYNWEPEPSDPYGHEDCVEMLSGRWNDECHLTMYFVCEFFKK
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CDS
ORIGIN
Query Match      41.1%; Score 655.8; DB 10; Length 867;
Best Local Similarity 85.2%; Pred. No. 5.6e-156;
Matches 732; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
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b 4 CAGTCAATGATGCTTGGTTCATCTTGGTTCGAGAAACCAATTTATCTCTCTGCTACTAG 63
Y 61 TTCTTTTGCATTTAGAGTCTGGTTCGATTTATGATAGCGCTCTACCTGCTGAGTCT 120
b 64 CTCTCTTGCATTTAGAGTCTGGTTCGATTTATGATAGCGCTCTACCTGCTGAGTCT 123
Y 121 GTGCCACACACAAATTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
b 124 GTGCCACACATACATTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 183
Y 181 GAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
b 184 GAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Y 241 TGGGTGATATGGAGATCGGGGCAATTTGGCAAGACTGGGGCCATTTGGGAGAGGGTG 300
b 244 TGGGTGATATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
Y 301 ACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
b 304 ACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
Y 361 GTGATTTGGAGATACCGGAAATTTGGTGGACAACTGGATATAGTATTTGCCCGGCTCA 420
b 364 GTGATTTGGCAGGTACCGGAAATTTGGTGGACAACTGGATATAGTATTTGCCCGCTTA 423
Y 421 AGACATCTATGAATTTGTCAAGAAATGTATAGCAGGAGGAGGAGGAGGAGGAGGAG 480
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Y 481 TCTACTACATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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Y 541 GGGGTGAGATCTAGCCATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
b 544 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 603
Y 601 TTGCCAAGAGTGGCTTTCTTGGGTGTTCAATTTGGCGTGAATGACCTTGAAGAGGAGGAG 660
b 604 TCGCCAAGAGTGGCTTTCTTGGGTGTTCAATTTGGCGTGAATGACCTTGAAGAGGAGGAG 663
Y 661 AGTACATGTTACAGAGCAACACTCCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
b 664 AATATGTTTACAGAGTAACTCCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 723
Y 721 CCAGCAGCCCTATGTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
b 724 CTAGTGACCCCTCCGGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 783
Y 781 ACAGAGTGGCCATCTTACCATGTTCTTGTCTGTGAGTTTCATCAGAGGAGGAGGAGGAG 840
b 784 ACAGAGTGGTTCATCTTACCATGTTCTTGTCTGTGAGTTTCATCAGAGGAGGAGGAGGAG 843
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b 844 TTTCTCATGTTACAGT 862

RESULT 8
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LOCUS AX410041 496 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2688 from Patent WO0229103.
ACCESSION AX410041
VERSION AX410041.1 GI:21442746
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

1
Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 2688 11-APR-2002;
GENE LOGIC INC (US)
Location/Qualifiers
1..496
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. N74624"

Query Match 22.5%; Score 358.2; DB 6; Length 496;
Best Local Similarity 96.8%; Pred. No. 3.8e-80;
Matches 387; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

QY 1198 TTACTCTGGTGATGATTAGGAAGGTTGTG--ATGTTAGGCTAACCTGCGCTGCCCAAA 1255
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QY 1256 G-CCAGACATGTACAAGGCTTTCTGTGAGCAATGATGAATCTTTGAATCCAAGATGCC 1314
Db 351 GCCAGACATGTACAAGGCTTTCTGTGAGCAATGATGAATCTTTGAATCCAAGATGCC 292
QY 1315 CAGATGTTTTCACAGTCAACCCATGCGCATGCTTACTTTGGAAGTTCTCTTGTGTTGG 1374
Db 291 CAGATGTTTTCACAGTCAACCCATGCGCATGCTTACTTTGGAAGTTCTCTTGTGTTGG 232
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RESULT 9
AC115924
LOCUS AC115924 166900 bp DNA linear HTG 18-JUN-2003
DEFINITION Mus musculus clone RP24-511011, WORKING DRAFT SEQUENCE, 4 ordered pieces.
ACCESSION AC115924 GI:31880195
VERSION AC115924.4
KEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 166900)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-511011
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166900)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukigalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, V., Collangelo, M., Collins, S., Collimore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hags, B., Horton, L., Hulme, W., Iliiev, I., Johnson, R., Jones, C., Khat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McSwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Milenda, T., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Plunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 166900)

REFERENCE
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelkail, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boquist, A., Bouchgalter, B., Camarata, J., Chang, J., Choepel, Y., Collimore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Faro, S., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Milenda, T., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Plunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (18-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 18, 2003 this sequence version replaced gi:21490462.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 124895
Center clone name: 511_O_11

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165673 bases at least Q40
Consensus quality: 166156 bases at least Q30
Consensus quality: 166365 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 166600; sum-of-contigs
Quality coverage: 13.2 in Q20 bases; agarose-fp
Quality coverage: 12.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 48320: contig of 48320 bp in length

* 48321 48420: gap of 100 bp
* 48421 59799: contig of 11379 bp in length
* 59800 59899: gap of 100 bp
* 59900 135830: contig of 75931 bp in length
* 135831 135930: gap of 100 bp
* 135931 166900: contig of 30970 bp in length.
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1. 48320
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vector_side:left
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/notes="assembly_fragment"
59900..135830
/notes="assembly_fragment"
135931..166900
/notes="assembly_fragment"
clone_end:T7
vector_side:right

ORIGIN

Query Match 21.68; Score 344.4; DB 2; Length 166900;
Best Local Similarity 82.38; Pred. No. 1.2e-76;
Matches 408; Conservative 0; Mismatches 86; Indels 2; Gaps 1;
QY 447 CTGTATGACAGGATTTAGGAACTGAGAGAAATTTCTATCATCTGTCAGGAGGAGAG 506
Db 15148 GTTATAGCAGGATCCGGAACTGAGAGAAATTTCTATCATCTGTCAGGAGGAGAG 15207
QY 507 AACTACAGGATCCCTTAACCCACTGCAGGATTCGGGGTGGATGCTAGCCATGCCCAAG 566
Db 15208 AACTACAGGATCTCTGACCCCACTGCAGGATCCGAGAGGGATGCTAGCCATGCCCAAG 15267
QY 567 GATGAAGTGCACACACACTCATGCTGACTATGTTGCCAAGAGTGGCTTCTTTGGGGTG 626
Db 15268 GATGAAGTGCCTTACACCCCTTATTGCTGACTATGTCGCCAAGAGTGGCTTCTTTACAGAGTG 15327
QY 627 TTCATTGCGTGAATGACCTTGAAGGGAGGAGGACAGTACATGTTTCACACACACATCCA 686
Db 15328 TTCATTGCGGTCATGACCTTGAAGGGAGGAGGACAGTACATGTTTCACACACATCCA 15387
QY 687 CTGCAGAACTATAGCAACTGGATAGGGGGGAAACCCAGCCACCCCTATGTCATGAGGAC 746
Db 15388 TTGCAGAACTATAGCAACTGGATAGGGGGGAAACCCAGCCCTCCGCGCATGAGGAC 15447
QY 747 TGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTCCCATCTTACCATGTAC 806
Db 15448 TGTGTGGAGATGTTGAGCTCTGGCAGATGGAATGACACAGAGTCCCATCTTACCATGTAT 15507
QY 807 TTTGTCTGTGAGTTTCATCAAGAGAGAGAGTAACTTCCCTCATCCTACGTAATTTGCTATT 866
Db 15508 TTTGTCTGTGAGTTTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 15567
QY 867 TTCCTGTGACCGCTATTCAGTATTGCTTATCCATCCCTTTTTTCTGATGTTACTACAT 926
Db 15568 TCCTCTGGGTC--TCCTAGTAGTCACTTTTATCCATCTTTGCTTCCCTTCTTATCATGCTT 15625
QY 927 TTGATCTCAGTCAACA 942
Db 15626 TTGCTCAATGCCATA 15641

RESULT 10
AC123656

LOCUS
DEFINITION
AC123656 222510 bp DNA linear HTG 27-MAR-2003
Mus musculus clone RP23-188M21, WORKING DRAFT SEQUENCE, 6 unordered
pieces.


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2y 687 CTGCAGAACTATAGCAACTGGAATGGGGGGAACCCAGGAGACCCCTTATGGTCATGAGGAC 746
db 157440 TTGCAGAACTACAGCAACTGGAGGAGGAGGAACCTAGTGACCCCTCCGGCCATGGGAC 157499
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2y 807 TTTGCTGTGTGAGTTTCATCAAGAGAAAGAAAGTAACTTCCCTCATCTCCATGCTATTGCTATT 866
db 157560 TTTGCTGTGTGAGTTTTCATCAAGAGAAAGAAATATTTTCCCTCATGTTACACAGTCACTT 157619
2y 867 TTCCTGTGACCGTCATTACAGTATTGTTATCCATCCCTTTTTCCTGATGTTACTACAT 926
db 157620 TCCCTGGGTC--TCTAGTAGTACATCTTTTATCCATCTTTGCTTCCCTTCTAATTACATTGCTT 157677
2y 927 TTGATCTGAGTCAACA 942
db 157678 TTGCTCAATGCCATA 157693

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RESULT 11
AC131337 345420 bp DNA linear HTG 23-APR-2003
LOCUS Mus musculus clone RP23-480E1, WORKING DRAFT SEQUENCE, 17 unordered
DEFINITION
ACCESSION AC131337
VERSION AC131337.4 GI:30017797
KEYWORDS HTG; HTGS, PHASE1; HTGS, DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345420)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-480E1
Unpublished
2 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cooke,A., Cooke,P., Corum,B., DeArrellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,

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Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramaesam,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 17, 2003 this sequence version replaced gi:28626850.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26504
Center clone name: 480_E_1

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NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 13581 19224: contig of 5544 bp in length
* 19225 19324: gap of 100 bp
* 19325 24245: contig of 4921 bp in length
* 24246 24345: gap of 100 bp
* 24346 33304: contig of 8959 bp in length
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* 33405 43959: contig of 10555 bp in length
* 43960 64192: contig of 20133 bp in length
* 64193 64292: gap of 100 bp
* 64293 140233: contig of 75941 bp in length
* 140234 140333: gap of 100 bp
* 140334 166937: contig of 26604 bp in length
* 166938 167037: gap of 100 bp
* 167038 202564: contig of 35527 bp in length
* 202565 202664: gap of 100 bp
* 202665 235865: contig of 33201 bp in length
* 235866 235966: contig of 100 bp
* 235967 282239: contig of 45274 bp in length
* 282240 282339: gap of 100 bp
* 282340 325240: contig of 42901 bp in length
* 325241 325340: gap of 100 bp
* 325341 345420: contig of 20080 bp in length.

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RIGIN

Query Match 21.6%; Score 344.4; DB 2; Length 345420;
Best Local Similarity 82.3%; Pred. No. 1.2e-76;
Matches 408; Conservative 0; Mismatches 86; Indels 2; Gaps 1;
Y 447 GTGATGAGGGGATTAGGAAATCGAAGAAATCTACTATCGTCGCGAGAGAGAGAG 506
b 176225 GTTATAGCAGGATCCGGAACTCGGAACTGAAGAAATCTACTATGTCGAGGAGAG 176284
Y 507 AACTACAGGAAATCCCTAACCCACTCAGGATTCGGGTGGAAATGCTAGCCATGCCAG 566
b 176285 AACTACAGGAAATCTCTGACCCACTGCAGGATCCGAGGAGGATGCTAGCCATGCCAG 176344
Y 567 GATGAAGTCGCCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTCGGGTG 626
b 176345 GATGAAGTCGTTAACACCTTATGCTGACTATGTCGCCAAGAGTGGTTCCTTCAGAGTG 176404
Y 627 TTCAATGGCGTGAATGACCTTGAAGAGGAGGACAGTACATGTTTCACAGAACACTCCA 686
b 176405 TTCAATGGCGTGAATGACCTTGAAGAGGAGGAGGAGTATGTTTCACAGAACACTCCA 176464
Y 587 CTCGAGAACTATAGCAACTGGAATGAGGGGAACCCAGCGCCCTATGTCATGAGGAC 746
b 176465 TTGCAAGAACTACAGCAACTGGAAGAGGAGGAGGAACTGATGACCCCTCGGCCATGAGGAC 176524
Y 747 TGTGTGAGATGCTGAGCTTCGTCAGATGGAATGACACAGAGTGCCATCTTACCATGTAC 806
b 176525 TGTGTGAGATGCTGAGCTTCGTCAGATGGAATGACACAGAGTGTCACCTTACCATGTAT 176584
Y 807 TTTGCTGTGAGTTCATCAGAGAAAGTAACTTCCCTCATCTCAGTATTTGCTATT 866
b 176585 TTTGCTGTGAGTTCATCAGAGAAAGTAAATTTTCCCTCATGTTACAGTACACCTT 176644
Y 867 TTCCTGTGACCGCTATACAGTATTTGTTATCCATCCTTTTTTCTGATGTACTACAT 926
b 176645 TCCCTGGGTC--TCCTAGTAGTCACTTTTATCCATCTTTGCTTCTTAATACATGTCTT 176702

QY 927 TTGATCTGAGTCAACA 942
Db 176703 TTGCTCAATGCCATA 176718

RESULT 12

AC097055 234922 bp DNA linear HTG 15-NOV-2002
LOCUS Rattus norvegicus clone CH230-2P22, WORKING DRAFT SEQUENCE, 3
DEFINITION unordered pieces.
AC097055
VERSION AC097055.5 GI:25007102
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 234922)

REFERENCE

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Cartoll, L., Dederich, D.A.,
Dellaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Lucier, R., Luna, R., Ma, J.,
Lozano, R.J., Lu, X., Lucier, A., Martin, R., Martindale, A., Martinez, E.,
Maheshwari, M., Mapus, P., Martin, R., Meador, M., Mei, G., Metzger, M.,
Massey, E., Mathew, E., McLeod, M.P., Meadow, M., Morgan, M., Morris, S.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Mosier, M., Neal, Z., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saverly, G.,
Schärer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,
Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

TITLE

JOURNAL

2 (bases 1 to 234922)

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (06-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 234922)

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 15, 2002 this sequence version replaced gi:23664540.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: TUS

Center clone name: CH230-2F22

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 231210 bases at least Q40

Consensus quality: 232236 bases at least Q30

Consensus quality: 233086 bases at least Q20

Estimated insert size: 241867; sum-of-contigs estimation

Quality coverage: 11x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 186689: contig of 186689 bp in length

* 188690 188789: gap of unknown length

* 188790 232956: contig of 44167 bp in length

* 232957 233056: gap of unknown length

* 233057 234922: contig of 1866 bp in length.

----- Location/Qualifiers

FEATURES

source

1..234922

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-2F22"

ORIGIN

Query Match 21.5%; Score 343; DB 2; Length 234922;
Best Local Similarity 83.1%; Pred. No. 2.7e-76;
Matches 403; Conservative 0; Mismatches 80; Indels 2; Gaps 1;

QY 447 GTGATAGCAGGATAGGGAACCTGAAGAGAAATTTACTACATCGTCGAGGAGAGAAG 506
DB 14303 GTCATAGCAGGATCCGGGAACCTGAAGAGAAATTTACTACATTTGCGAGGAGAAAG 14362

QY 507 AACTACAGGGAATCCCTAACCCACTGAGGATTCGGGGTGAATGCTAGCCATGCCCAAG 566
DB 14363 AACTACAGGGAATCTCTGACCCACTGAGGATTCGGGGAGGATGCTGGGCATGCCCTAAG 14422

QY 567 GATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGCTCTTTCCGGGTG 626
DB 14423 GATGAAGTGTTTAACACTCTTATTGCTGACTATGTCGCCAAGAGTGGCTCTTTCAGAGTG 14482

QY 627 TTCATTGGCGTGAATGACCTTGAAGAGGAGGAGGACAGTACATGTTTCACAGACACACTCCA 686
DB 14483 TTCATTGGCGTGAATGACCTTGAAGAGGAGGAGGACAGTACATGTTTCACAGACACACTCCA 14542

QY 687 CTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCCGCCCTATGCTCATGAGGAC 746

Db 14543 TTCCGAACCTACAGCAACTGGAAGAGGGGAGCCTAGTACCCCTATGGCATGAGGAC 14602
QY 747 TGTGTGGAGATGCTGAGCTCTCGCAGATGGAATACAGAGTGCCTCTTACCATGTAC 806
Db 14603 TGTGTGGAGATGCTGAGCTCTCGCAGAGTGGAAACAGACAGAGTGTCTTACCATGTAT 14662
QY 807 TTTGTCTGTGAGTTTCATCAAGAAGAAAAGTAACTTCCTCATCTCTAGCTATTTTCTATT 866
Db 14663 TTTGTCTGTGAGTTTTCATCAAGAAGAAAATTAATTTCTTCATGTTACACAGGCACTTC 14722
QY 867 TTCTGTGACCGTCATTACAGTTATTTGTTATCCATCCCTTTTTTCTCTGATGTACTACAT 926
Db 14723 TCCAGGGTCT--TCCTAGCAGTTACTTTTATTTCATTGTTGCTTTCTAACTTCATTGAT 14780
QY 927 TTGAT 931
Db 14781 TTGCT 14785

RESULT 13

BC056052

LOCUS

DEFINITION

Xenopus laevis collectin sub-family member 11, mRNA (cDNA clone

MGC:89012 IMAGE:4963954), complete cds.

ACCESSION

BC056052

VERSION

BC056052.1 GI:33417123

KEYWORDS

MGC.

SOURCE

Xenopus laevis

ORGANISM

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 1272)

Klein, S.W., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.

and Richardson, P.

Genetic and genomic tools for Xenopus research: The NIH Xenopus

initiative

Dev. Dyn. 225 (4), 384-391 (2002)

JOURNAL

DEV. DYN. 225 (4), 384-391 (2002)

MEDLINE

2234132

PUBMED

12454917

REFERENCE

2 (bases 1 to 1272)

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scapleton, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Loquellano, N.A., Peters, G.J.,

Carninci, P., Prange, C., Raha, S.S., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Sanchez, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

Boiffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

PROC. NATL. ACAD. SCI. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE

22388257

PUBMED

12477932

REFERENCE

3 (bases 1 to 1272)

Klein, S. and Strausberg, R.

Direct Submission

Submitted (01-AUG-2003) National Institutes of Health, Xenopus Gene

Collection (XGC), National Institute of Child Health and Human

Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD

20892-7510, USA

NIH-MGC Project

REMARK

COMMENT

Contact: XGC help desk
 Email: cgahe-remail.nih.gov
 Tissue Procurement: Dr. Igor Dawid
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK plate: 129 Row: 1 Column: 1
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

FEATURES

Location/Qualifiers
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 /db_xref="taxon:8355"
 /clone="MGC:69012 IMAGE:4963954"
 /tissue_type="Spleen, adult Xenopus"
 /clone_lib="NICHID_XGC_Spl"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

gene

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 /gene="colecl1-prov"
 /note="synonym: MGC69012"
 /db_xref="locusID:380029"
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misc_feature

/note="(CLECT; Region: C-type lectin (CTL) and CTL-like domains"
 /db_xref="CDD:cd00037"

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 Best Local Similarity 59.1%; Pred. No. 3.3e-57;
 Matches 476; Conservative 0; Mismatches 328; Indels 1; Gaps 1;

Y 82 TGGGTCTGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCCACACACACATTTTAC 141
 b 166 TGGATCTGGATATTGTCAGCATATC-ACAGATGAGACATGTTCTGTGAGATATTGTCC 224
 Y 142 CAGGACCCAAAGAGATGATGTGAAAGAGAGATCCAGGAGAGAGAGAAAGCATGGCA 201
 b 225 CTGGTCTGAAAGAGATGCGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 284
 Y 202 AATGGGACGCAATGGGCGGCAAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
 b 285 GAGTTGGCCCTCTCGGGGAAAAGGGAGAAATTTGGGATAAAGAGAAAGAGAGAGATGG 344
 Y 262 GCAATATTGCAAGATGCGGCCCATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 321
 b 345 GTCGTCTGAAAGATTTGGTCTATTGGTTCGAAAGGTGAAAGAGAGAGAGAGAGAG 404
 Y 322 TTGGAATACCTGGAGAAAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 381
 b 405 TCGGCCCTCAGGACCAATATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 464

QY 382 AATTTGTTGGACAACTGGATATTAGTATTCCTCCGGCTCAAGACATCTATGAAGTTTGTCA 441
 Db 465 AAGCTGTTGGAGAAATGACATCAAGTTCTCTCAGCTGGCTACAGAAGTGAAATTTGTGA 524
 QY 442 AGAATGATAGCAGGAGATTTAGGAAACTCAAGAAATTTCTACTACATCGTCGAGGAG 501
 Db 525 AAAATGTTGTTGTTGGAGTCCGAGAGACGGAGACAAAATCTATCTTCTGTTGGAAGAAG 584
 QY 502 AGAAGAACTACAGGGAATCCCTAAACCACATGCAGGATTCGGGGTGGAAATGCTAGCCATGC 561
 Db 585 AGAAGAGTACATTGATGCCAGGACTACTGCCAGGAGAGAGGTGGGACCTCAGCATGC 644
 QY 562 CCAGGATGAAGCTGCCACACACATCTATCCTGACTATGTTGCCAAGAGTGGCTTTTTC 621
 Db 645 CTAAGGATGAGCAACTAATAGTTTGAATTCCTCTTACATTAATCATGCTGGCTCTCAA 704
 QY 622 GGGTGTTCATTGGCGTGAATGACCTTCAAGAGGAGGAGACAGTACATGTTTCACAGACAA 681
 Db 705 GAGTGTTCATTGGGATCAATGACTTGGAAAGAGAGGCCACTTTGTGTATTCGATCGCT 764
 QY 682 CTCACATGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGGAGCCCTATGGTCATG 741
 Db 765 CTCATATGCAGACCTTCAATAAATGGCGCCAGGAGAGAGAGAGAGAGAGAGAGAGAG 824
 QY 742 AGGACTGTGTGAGATGCTGAGCTCTGCGAGATGGAATGACACAGAGTGCATCTTACCA 801
 Db 825 AAGACTGTGCTGAGATGTTTCATCCGGGGATGGAATGATGTTTCTGCTTATTACTA 884
 QY 802 TGTACTTTGCTGTGAGTTCATCAAGAGAAAGTAACTTCCTCATCTCCTATGTTG 861
 Db 885 TGTATTTTATTGTTGAGTTTGATAAAGAAATGTATACTGTCTCAAAATTTCTAACATGA 944
 QY 862 CTATTTTCTGCTGACCGCTCATTACA 886
 Db 945 CCAATCATATGTTATAGCATGGCA 969

RESULT 14
 AR252616
 LOCUS 1238 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 356 from patent US 6478825.
 ACCESSION AR252616
 VERSION AR252616.1 GI:27300524
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1238)
 AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
 TITLE Implant, method of making same and use of the implant for the
 treatment of bone defects
 JOURNAL Patent: US 6478825-A 356 12-NOV-2002;
 FEATURES
 source
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 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 15.4%; Score 246; DB 6; Length 1238;
 Best Local Similarity 58.4%; Pred. No. 1.5e-51;
 Matches 429; Conservative 0; Mismatches 305; Indels 0; Gaps 0;

QY 106 CTACCGCTGAAGTCTGTGCCACACACACAAATTTCCAGGAGCCCAAGAGAGATGATCGTG 165
 Db 149 CTGGCGATGACCCCTGCTCTGTGAGATCTCTGCTCCCTCGGCTCAAGGGGATCGGGAG 208
 QY 166 AAAAGAGAGATCCAGGAG 225
 Db 209 AGAAGGAGACAAAGGCGCCCGGAGCGCTGGAAGAGTCCGCCCAAGAGAGAGAGAG 268
 QY 226 GAATTAAGAGAGAACTGGGTGATGATGAGAGATCGGGCAATATTGGCAAGACTGGCCCA 285
 Db 269 GAGACATGGGGAGCAAAAGGAGACAGAAAGGAGCGATGTTGGTCTGCTATGGAAATTTGTTCCCA 328

286 TTGGAGAGAGCGGTGACAAAGGGGAAAAAGCTTTGCTTGGAAATCTCTGGAGAAAAAGGCA 345
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329 TTGGCTCTAAAGGTGAGAAAGGAGATTCGGTGACATAGGACCCCTTGTCTCTAATGGAG 388
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346 AAGCAGGTACTGTCTGTGATTTGTGGAAGATACCGGAAATTTGTGACAACTCTGATATTA 405
347
389 AACAGGCTCCCACTGTGAGTGCAGCGAGCTGCGAAGCCATCGGGAGATGGACAACC 448
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406 GTATTGCCCGGCTCAAGACATCTATGAGTTTGTCAAGATGTGATAGCAGGATAGGG 465
407
449 AGGTCTCTCAGCTCAGCAGGAGCTCAAGTTTCATCAAGAAATGTGTCGCGGTGTGCGG 508
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466 AAACCTGAAGAGAAATTTCTACTACATCTGCGAAGAGAGAACTACAGGGAATCCCTAA 525
467
509 AGACGAGAGCAAGATCTACTCTGCTGTGAGGAGGAGAGCGCTACGCGAGCGCCAGC 568
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526 CCCACTGAGAGATTCGGGGTGGAAATGTACCCATGCCAAGAGTGAAGTGCACACAC 585
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646 TTGAAAGGAGGAGGACAGTACATGTTTCACAGACAACTCCACTGCAGAACTATAGCACT 705
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750
766 CTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTTGCTGTGATTCATCA 825
767
809 CGGGGCGCTGGAACGACGTGGCTGCGACACCACTGATGTAATCATGTGTGATTTGACA 868
808
826 AGAAGAAAAGTAA 839
827
869 AGGAGAACATGTGA 882

RESULT 15
AX403469 1238 bp DNA linear PAT 14-JUN-2002
LOCUS
DEFINITION Sequence 356 from Patent WO0073454.
ACCESSION AX403469
VERSION AX403469.1 GI:21436970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 356 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 15.4%; Score 246; DB 6; Length 1238;
Best Local Similarity 58.4%; Pred. No. 1.5e-51;
Matches 429; Conservative 0; Mismatches 305; Indels 0; Gaps 0;

106 CTACCGCTGAAGTCTGTGCCACACACAAATTTCCACAGGACCCCAAGAGAGATGATGGT 165
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149 CTGGCGATGACGCTGCTCTGTGCAGATCCCTCGTCCCTCAAAGGGGATCGGGAG 208
150
166 AAAAGGAGATCCAGAGAGAGGAAAGCATGCGAAATGTGGAGCGATGGGGCCGAAAG 225
167
209 AGAAGGAGACAAAAGGCGCCCGGACGCGCTGGAGAGATCGGCCCCACGGGAGAAAAAG 268
210
226 GAATTTAAAGGAGAACTGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCA 285
227
269 GAGACATGGGGAGCAAGAGACAGAAAGGCGATGTGGGTGCTCATGTGAAAAATTTGGTCCCA 328
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286 TTGGGAGAGAGGTGACAAAAGGGGAAAAAGTTTCTTGGAAATCTCTGGAGAAAAAGGCA 345
287
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346 AAGCAGGTACTGTCTGTGATTTGTGGAAGATACCGGAAATTTGTGGAACAACTGGATATTA 405
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389 AACAGGCTCCCACTGTGAGTGCAGCGAGCTGCGAAGCCATCGGGAGATGGACAACC 448
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407
449 AGGTCTCTCAGCTGACGAGCGAGCTCAAGTTTCATCAAGAAATGCTGTGCGCGGTGTGCGG 508
450
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646 TTGAAAGGAGGAGGACAGTACATGTTTCACAGACAACTCCACTGCAGAACTATAGCACT 705
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750
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767
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Job time : 6256 secs

GenCore version 5.1.6
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4 nucleic - nucleic search, using sw model

in on: February 23, 2004, 19:06:31 ; Search time 652 Seconds

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file: US-09-600-932-1

effect score: 1595
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Gapop 10.0 , Gapext 1.0

arched: 3373863 seqs, 2124099041 residues

total number of hits satisfying chosen parameters: 6747726

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqm1990as: *
3: geneseqm2000as: *
4: geneseqm2001as: *
5: geneseqm2001bs: *
6: geneseqm2002as: *
7: geneseqm2003as: *
8: geneseqm2003bs: *
9: geneseqm2003cs: *
10: geneseqm2004as: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1595	100.0	1595	2	Aax88323 Human col
2	980.2	61.5	1016	2	Aaz33973 Human PRO
3	980.2	61.5	1016	3	Aac78480 Human PRO
4	980.2	61.5	1016	4	Aas45974 Human DNA
5	980.2	61.5	1016	7	ABX78577 Human PRO
6	980.2	61.5	1016	7	ACA75549 Novel hum
7	980.2	61.5	1016	7	ACA71029 Human sec
8	980.2	61.5	1016	7	ACC87557 Human sec
9	980.2	61.5	1016	7	ACC86943 Human sec
10	980.2	61.5	1016	7	ACD04116 Human sec
11	980.2	61.5	1016	7	ACA69447 cDNA enco
12	980.2	61.5	1016	7	ACA90292 Novel hum
13	980.2	61.5	1016	7	ACC83399 Human sec
14	980.2	61.5	1016	7	ACA98190 Novel hum
15	980.2	61.5	1016	7	ACA93832 Human sec
16	980.2	61.5	1016	7	ACD15225 Human sec
17	980.2	61.5	1016	7	ACD08812 Human sec
18	980.2	61.5	1016	7	ACC96732 Human sec
19	980.2	61.5	1016	7	ACF15453 Human sec
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21	980.2	61.5	1016	7	ACA72820 Human PRO
22	980.2	61.5	1016	7	ACC02992 Novel hum
23	980.2	61.5	1016	7	ACD01807 Novel hum

ALIGNMENTS

RESULT 1
AAX88323
ID AAX88323 standard; cDNA; 1595 BP.

XX
AC AAX88323;
DT 30-SEP-1999 (first entry)
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DE Human collectin cDNA.
XX
KW Collectin; human; antibacterial; antiviral; treatment; infection; ds.
XX Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 6..839
FT /*tag= a
FT /product= "collectin"
XX
PN WO9937767-A1.
XX
PD 29-JUL-1999.
XX
PF 24-JUL-1998; 98WO-JP003328.
XX
PR 23-JAN-1998; 98JP-00011281.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N;
XX
DR WPI; 1999-458691/38..
DR P-PSDB; AA25518.
XX
PT New collectin protein of human origin and DNA encoding it.
XX
PS Claim 2; Page 39-42; 58pp; Japanese.
XX
CC This invention describes the isolation and characterisation of a novel
CC human collectin protein and its encoding polynucleotide. The human
CC collectin exhibits antibacterial and antiviral activity and can be used
CC as an agent for the treatment of human bacterial and viral infections.
CC This sequence encodes the novel human collectin
XX
SQ Sequence 1595 BP; 444 A; 322 C; 382 G; 447 T; 0 U; 0 Other;

Aca91999 Novel hum
Aca63541 Novel hum
Aca89424 cDNA enco
Aca73434 Human sec
Aca05749 Human sec
Aca66583 cDNA enco
Acf20158 Human sec
Acf19544 Human sec
Acf12997 Human sec
Acd25100 Human sec
Acf00149 Human sec
Aca72206 Novel hum
Acd04730 Novel hum
Acd18191 Human sec
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Acd12296 Novel hum
Acc74211 Human sec
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Query Match				100.0%; Score 1595; DB 2; Length 1595;			
Best Local Similarity				100.0%; Pred No. 0;			
Matches 1595; Conservative				0; Mismatches 0; Indels 0; Gaps 0;			
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2b	1	CAGCAATGAATGGCTTTGCAATCCCTTGGCTTCGAAAGAACCAATTTATCTCTCGGTACTAT	60				
2Y	61	TTCTTTTGGCAATTCAGAGCTCGGGCTGGATATTTGATAGCGTCTACCGTGAAGTCT	120				
2b	61	TTCTTTTGGCAATTCAGAGCTCGGGCTGGATATTTGATAGCGTCTACCGTGAAGTCT	120				
2Y	121	GTGCCACACACAAATTCACAGAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAG	180				
2b	121	GTGCCACACACAAATTCACAGAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAG	180				
2Y	181	GAGAGAGGGAAGCATGGCAAGTGGAGCGCATGGGCGGCAAGGAATTAAGGAGAC	240				
2b	181	GAGAGAGGGAAGCATGGCAAGTGGAGCGCATGGGCGGCAAGGAATTAAGGAGAC	240				
2Y	241	TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCAATTGGGAAGAGGTG	300				
2b	241	TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCAATTGGGAAGAGGTG	300				
2Y	301	ACAAGGGGAAGAGTTTGGTGGATACCTGGAGAAAGCAAGCAGGTACTGTCT	360				
2b	301	ACAAGGGGAAGAGTTTGGTGGATACCTGGAGAAAGCAAGCAGGTACTGTCT	360				
2Y	361	GTGATTTGGGAAGTACCGGAATTTCTTGGCAAACTGGATATTAGTATTGCCCGGCTCA	420				
2b	361	GTGATTTGGGAAGTACCGGAATTTCTTGGCAAACTGGATATTAGTATTGCCCGGCTCA	420				
2Y	421	AGACATCTAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAAAT	480				
2b	421	AGACATCTAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAAAT	480				
2Y	481	TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAAACCCACTGCAGGATTC	540				
2b	481	TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAAACCCACTGCAGGATTC	540				
2Y	541	GGGGTGGGAATGTAGCCATGCCAAGATGAAGCTGCCAACAACACTCATCGCTGACTATG	600				
2b	541	GGGGTGGGAATGTAGCCATGCCAAGATGAAGCTGCCAACAACACTCATCGCTGACTATG	600				
2Y	601	TTGCCAAGAGTGGCTTTCTTCGGGTGTTCAATGGCGTGAATGACCTTGAAGAGAGGGAC	660				
2b	601	TTGCCAAGAGTGGCTTTCTTCGGGTGTTCAATGGCGTGAATGACCTTGAAGAGAGGGAC	660				
2Y	661	AGTACATGTTCAAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC	720				
2b	661	AGTACATGTTCAAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC	720				
2Y	721	CCAGGACCCCTATGGTCAAGAGACTGTGTGAGATGCTGAGCTTGGCAGATGGAATG	780				
2b	721	CCAGGACCCCTATGGTCAAGAGACTGTGTGAGATGCTGAGCTTGGCAGATGGAATG	780				
2Y	781	ACACAGAGTGCATTTACCATGTTCTGTGTGAGTTTCAATCAAGAGAAAGAAATTAAC	840				
2b	781	ACACAGAGTGCATTTACCATGTTCTGTGTGAGTTTCAATCAAGAGAAAGAAATTAAC	840				
2Y	841	TTCCCTCATCTACGATTTTCTGATTTTCTGTGACCGCTCATACAGTTATTTGTTATCA	900				
2b	841	TTCCCTCATCTACGATTTTCTGATTTTCTGTGACCGCTCATACAGTTATTTGTTATCA	900				
2Y	901	TCCTTTTTTCTGATTTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA	960				
2b	901	TCCTTTTTTCTGATTTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA	960				
2Y	961	CTGAGGTATGAGCCCTCCATCATGCTCTTTTGTGATGATTTTCAATTTTTCACAT	1020				
2b	961	CTGAGGTATGAGCCCTCCATCATGCTCTTTTGTGATGATTTTCAATTTTTCACAT	1020				
2Y	1021	GGTATGTTATTGACCCCAATAACTCGCCAGGTTACATGGGCTTTGAGAGAGAAATTTAATT	1080				

Db	1021	GGTATGTTATTGACCCCAATAACTCGCCAGGTTACATGGTCTTGAGAGAGAAATTTAATT	1080
Qy	1081	ACTAATTTGCGACGAGATAGTTGGTTGCTATATGTCAAATGAGTTGTTCTCTTGGTATT	1140
Db	1081	ACTAATTTGCGACGAGATAGTTGGTTGCTATATGTCAAATGAGTTGTTCTCTTGGTATT	1140
Qy	1141	TGCTCTACCATCTCTCCCTAGAGCACTCTGTCTCTATCCAGTGGATAATTTCCCGAGTTT	1200
Db	1141	TGCTCTACCATCTCTCCCTAGAGCACTCTGTCTCTATCCAGTGGATAATTTCCCGAGTTT	1200
Qy	1201	ACTGGTGATGATTAGGAAGTTTGTGATGGTTAGGCTAACCTGGCCCTGGCCCAAGCCAG	1260
Db	1201	ACTGGTGATGATTAGGAAGTTTGTGATGGTTAGGCTAACCTGGCCCTGGCCCAAGCCAG	1260
Qy	1261	ACATGTACAAAGGGCTTTCTGTGAGCAATGATAAGATCTTTGAATCCAAGATGCCCAGATG	1320
Db	1261	ACATGTACAAAGGGCTTTCTGTGAGCAATGATAAGATCTTTGAATCCAAGATGCCCAGATG	1320
Qy	1321	TTTTACAGTCAACCCCTATGGCCATGGCTATACCTTGTGAAAGTTCTCTTGTGGCACA	1380
Db	1321	TTTTACAGTCAACCCCTATGGCCATGGCTATACCTTGTGAAAGTTCTCTTGTGGCACA	1380
Qy	1381	CATAGAAATGCTTTTAACCCCAAGCCCTTATATGGGGACTTCTAGCTTTGTCTTGT	1440
Db	1381	CATAGAAATGCTTTTAACCCCAAGCCCTTATATGGGGACTTCTAGCTTTGTCTTGT	1440
Qy	1441	CAGACATGTGGAATGATAAATCTCTTTTGTCTTGTGATCTATGATTTCACTAACA	1500
Db	1441	CAGACATGTGGAATGATAAATCTCTTTTGTCTTGTGATCTATGATTTCACTAACA	1500
Qy	1501	TATACCAAGTAGTGCTTTTGAACCCCTTCTAGCTCACACCTTAATCTCAGGCCCT	1560
Db	1501	TATACCAAGTAGTGCTTTTGAACCCCTTCTAGCTCACACCTTAATCTCAGGCCCT	1560
Qy	1561	ATATAGTCACTTTGATTAAAGAAAACGGAGCC	1595
Db	1561	ATATAGTCACTTTGATTAAAGAAAACGGAGCC	1595
RESULT 2			
AAZ33973			
ID	AAZ33973 standard; cDNA; 1016 BP.		
XX	AAZ33973;		
AC	(first entry)		
XX	Human PRO702 nucleotide sequence.		
DE	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;		
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;		
KW	secreted protein; transmembrane protein; ss.		
XX	Homo sapiens.		
OS	99WO-US005028.		
XX	WO9946281-A2.		
PN	16-SEP-1999.		
PD	08-MAR-1999;		
XX	98US-0077450P.		
PF	98US-0077632P.		
XX	98US-0077641P.		
PR	98US-0077649P.		
PR	98US-0077791P.		
PR	98US-0078004P.		
PR	98US-00040220.		
PR	98US-0078866P.		
PR	98US-0078910P.		
PR	98US-0078936P.		
PR	98US-0078939P.		

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R 25-MAR-1998; 98US-0079294P.
R 26-MAR-1998; 98US-0079656P.
R 27-MAR-1998; 98US-0079663P.
R 27-MAR-1998; 98US-0079664P.
R 27-MAR-1998; 98US-0079689P.
R 27-MAR-1998; 98US-0079728P.
R 27-MAR-1998; 98US-0079786P.
R 30-MAR-1998; 98US-0079920P.
R 30-MAR-1998; 98US-0079923P.
R 31-MAR-1998; 98US-0080105P.
R 31-MAR-1998; 98US-0080107P.
R 31-MAR-1998; 98US-0080165P.
R 31-MAR-1998; 98US-0080194P.
R 01-APR-1998; 98US-0080327P.
R 01-APR-1998; 98US-0080328P.
R 01-APR-1998; 98US-0080333P.
R 01-APR-1998; 98US-0080334P.
R 08-APR-1998; 98US-0081049P.
R 08-APR-1998; 98US-0081070P.
R 08-APR-1998; 98US-0081071P.
R 09-APR-1998; 98US-0081195P.
R 09-APR-1998; 98US-0081203P.
R 09-APR-1998; 98US-0081229P.
R 15-APR-1998; 98US-0081617P.
R 15-APR-1998; 98US-0081838P.
R 15-APR-1998; 98US-0081955P.
R 15-APR-1998; 98US-0082568P.
R 21-APR-1998; 98US-0082569P.
R 21-APR-1998; 98US-0082700P.
R 22-APR-1998; 98US-0082704P.
R 22-APR-1998; 98US-0082804P.
R 23-APR-1998; 98US-0082767P.
R 23-APR-1998; 98US-0082796P.
R 27-APR-1998; 98US-0083336P.
R 28-APR-1998; 98US-0083322P.
R 29-APR-1998; 98US-0083392P.
R 29-APR-1998; 98US-0083495P.
R 29-APR-1998; 98US-0083496P.
R 29-APR-1998; 98US-0083499P.
R 29-APR-1998; 98US-0083500P.
R 29-APR-1998; 98US-0083545P.
R 29-APR-1998; 98US-0083554P.
R 29-APR-1998; 98US-0083558P.
R 29-APR-1998; 98US-0083559P.
R 30-APR-1998; 98US-0083742P.
R 05-MAY-1998; 98US-0084366P.
R 06-MAY-1998; 98US-0084414P.
R 06-MAY-1998; 98US-0084441P.
R 07-MAY-1998; 98US-0084598P.
R 07-MAY-1998; 98US-0084600P.
R 07-MAY-1998; 98US-0084627P.
R 07-MAY-1998; 98US-0084637P.
R 07-MAY-1998; 98US-0084639P.
R 07-MAY-1998; 98US-0084640P.
R 07-MAY-1998; 98US-0084643P.
R 13-MAY-1998; 98US-0085323P.
R 13-MAY-1998; 98US-0085338P.
R 13-MAY-1998; 98US-0085339P.
R 15-MAY-1998; 98US-0085573P.
R 15-MAY-1998; 98US-0085579P.
R 15-MAY-1998; 98US-0085580P.
R 15-MAY-1998; 98US-0085582P.
R 15-MAY-1998; 98US-0085689P.
R 15-MAY-1998; 98US-0085697P.
R 15-MAY-1998; 98US-0085700P.
R 15-MAY-1998; 98US-0085704P.
R 18-MAY-1998; 98US-0086023P.
R 22-MAY-1998; 98US-0086392P.
R 22-MAY-1998; 98US-0086414P.
R 22-MAY-1998; 98US-0086430P.
R 22-MAY-1998; 98US-0086486P.
R 28-MAY-1998; 98US-0087099P.

PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX (GETH ) GENENTECH INC.
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX MPI; 1999-551358/46.
XX P-PSDB; AAY41698.
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.
XX Claim 2; Fig 36; 530pp; English.
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to
XX AA41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention
XX
XX Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;

Query Match 61.5%; Score 980.2; DB 2; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.1e-279;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAATGAATGGCTTTGTCATCTTGTTCGAGAAACCAATTTATCTCTGCTGCTAT 60
Db 17 CAGCAATGAATGGCTTTGTCATCTTGTTCGAGAAACCAATTTATCTCTGCTGCTAT 76
QY 61 TTCCTTTGCAATTCAGAGTCGGGTCTGGATTTGATAGCCGTCCTACCGTGAAGTCT 120
Db 77 TTCCTTTGCAATTCAGAGTCGGGTCTGGATTTGATAGCCGTCCTACCGTGAAGTCT 136
QY 121 GTGCCACACACACATTTCCACGAGCCCAAGCAGATGATGGTGAAGAGGAGATCCAG 180
Db 137 GTGCCACACACACATTTCCACGAGCCCAAGCAGATGATGGTGAAGAGGAGATCCAG 196
QY 181 GAGAAGAGGGAAGCATGGCCAAAGTGGGACGCATGGGGCCGGAAGAAATTAAGGAGAAC 240
Db 197 GAGAAGAGGGAAGCATGGCCAAAGTGGGACGCATGGGGCCGGAAGAAATTAAGGAGAAC 256
QY 241 TGGGTGATATGGGAGATCGGGCAATATTGCGAGACTGGGCCCATTTGGGAAGAGGGTG 300
Db 257 TGGGTGATATGGGAGATCGGGCAATATTGCGAGACTGGGCCCATTTGGGAAGAGGGTG 316
QY 301 ACAAAAGGGGAAAAGGTTTGTTCGAATACCTCGAGAAAAGGCAAGCAGGTAAGTCTCT 360
Db 317 ACAAAAGGGGAAAAGGTTTGTTCGAATACCTCGAGAAAAGGCAAGCAGGTAAGTCTCT 376
QY 361 GTGATTGTGGAAGATACCGGAAAATTTGTTGGAACATCGGATATTAGTATTGCCCGGTCA 420
Db 377 GTGATTGTGGAAGATACCGGAAAATTTGTTGGAACATCGGATATTAGTATTGCCCGGTCA 436
QY 421 AGACATCTATGAATTTGTCGAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT 480
Db 437 AGACATCTATGAATTTGTCGAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT 496
QY 481 TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCGAGGATTC 540
Db 497 TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCGAGGATTC 556
QY 541 GGGGTGGATGCTAGCCATGCCAAGGATGAAGTGGCCACACACTCATGCTCAGCTATG 600
Db 541 GGGGTGGATGCTAGCCATGCCAAGGATGAAGTGGCCACACACTCATGCTCAGCTATG 600
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Db 557 GGGTGGGAATGCTAGCCATGCCAAGGATGAAGCTGCCACACACTCATCGCTGACTATG 616
QY 601 TTGCCAAGAGTGGCTTCTTTGGGTGTTTCATTCGCGTGAATGACCTTGAAGGAGGAC 660
Db 617 TTGCCAAGAGTGGCTTCTTTGGGTGTTTCATTCGCGTGAATGACCTTGAAGGAGGAC 676
QY 661 AGTACATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 720
Db 677 AGTACATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 736
QY 721 CCAGGACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTTCGGCAGATGGAATG 780
Db 737 CCAGGACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTTCGGCAGATGGAATG 796
QY 781 ACACAGAGTGCCATCTTACCATGACTTTGTCTGTGAGTTTCATCAAGAAAGAAAGTAAC 840
Db 797 ACACAGAGTGCCATCTTACCATGACTTTGTCTGTGAGTTTCATCAAGAAAGAAAGTAAC 856
QY 841 TTCCCTCATCTTACGTATTGCTATTTTCCTGTGACCGTCATACAGATTATGTTATCCA 900
Db 857 TTCCCTCATCTTACGTATTGCTATTTTCCTGTGACCGTCATACAGATTATGTTATCCA 916
QY 901 TCCCTTTTTCCTGATGTGCTACTACATTTGATCTGAGTCAACATAGCTAGAAATGCTAAA 960
Db 917 TCCCTTTTTCCTGATGTGCTACTACATTTGATCTGAGTCAACATAGCTAGAAATGCTAAA 976
QY 961 CTGAGGTATGGAGCTCCATCATCA 985
Db 977 CTGAGGTATGGAGCTCCATCATCA 1001

RESULT 3
AAC78480
ID AAC78480 standard; cDNA; 1016 BP.
XX
AC AAC78480;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO702 (UNQ366) nucleotide sequence SEQ ID NO:96.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
KW expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
PN WC200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WC-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 21-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028333.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 05-JAN-2000; 2000WO-US000277.
PR 05-JAN-2000; 2000WO-US000376.
XX
XX (GETH ) GENENTECH INC.
XX

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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Filyaroff E, Fong S, Gao W, Garber H, Gerritsen ME,
PI Goddard A, Godowski P, Grimaldi CJ, Gurney AL, Hillan KU, Shelton DL,
PI Kijavini ID, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Stewart TA,
PI Stewart TA, Williams D, Williams PM, Wood WI;
XX WPI; 2000-611443/58.
DR P-PSDB; AAB44254.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 2; Fig 36; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytotstatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
XX
Query Match 61.5%; Score 980.2; DB 3; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.le-279;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAATGAATGGCTTTGTCATCTTCTGCTCGAAGAAACCAATTTATCTCTCGTACTAT 60
Db 17 CAGCAATGAATGGCTTTGTCATCTTCTGCTCGAAGAAACCAATTTATCTCTCGTACTAT 76
QY 61 TTTCTTTTGCMAATTCAGAGTCTGGCTCTGGATATTGATAGCCGCTCTACCGTGAAGTCT 120
Db 77 TTTCTTTTGCMAATTCAGAGTCTGGCTCTGGATATTGATAGCCGCTCTACCGTGAAGTCT 136
QY 121 GTGCCACACACACAATTTCCAGGACCCAAAGAGATGATGTGTAAGAGAGATCCAG 180
Db 137 GTGCCACACACACAATTTCCAGGACCCAAAGAGATGATGTGTAAGAGAGATCCAG 196
QY 181 GAGAAGAGGGAACATGCGCAAGTGGGCGCATGGGCGGAAGGAATTTAAAGGAGAAC 240
Db 197 GAGAAGAGGGAACATGCGCAAGTGGGCGCATGGGCGGAAGGAATTTAAAGGAGAAC 256
QY 241 TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 300
Db 257 TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 316
QY 301 ACAAGGGGAAAAAGTTTCTTGGATACCTCGAAGAAAGCAAGCAGGTACTGTCT 360
Db 317 ACAAGGGGAAAAAGTTTCTTGGATACCTCGAAGAAAGCAAGCAGGTACTGTCT 376
QY 361 GTGATTGTGGAAGATACCGGAAATTTCTGGACAACCTGGATATTAGTATGCCCCCTCA 420
Db 377 GTGATTGTGGAAGATACCGGAAATTTCTGGACAACCTGGATATTAGTATGCCCCCTCA 436
QY 421 AGACATCTATGAAGTTTGTCAAGNATGTGATAGCGGATAGGGAACCTGAGAGAAAT 480
Db 437 AGACATCTATGAAGTTTGTCAAGNATGTGATAGCGGATAGGGAACCTGAGAGAAAT 496
QY 481 TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC 540
Db 497 TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC 556
QY 541 GGGGTGGAATCTAGCCATGCCCAAGGATGAAGTCCACACACACTCTGCTGACTATG 600
Db 557 GGGGTGGAATCTAGCCATGCCCAAGGATGAAGTCCACACACACTCTGCTGACTATG 616

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601 TTGCCAAGAGTGGCTCTTTTCGGGTGTTCAITGGCGTGAATGACCTTGAAAGGAGGGAC 660
617 TTGCCAAGAGTGGCTCTTTTCGGGTGTTCAITGGCGTGAATGACCTTGAAAGGAGGGAC 676
661 AGTACATGTTCCACAGACACTCCACTGCAGACTATAGCACTGGAATGAGGGGAAC 720
677 AGTACATGTTCCACAGACACTCCACTGCAGACTATAGCACTGGAATGAGGGGAAC 736
721 CCAGCGACCCCTATGGTCAATGAGGACTGTGGAGATCCTGAGCTCTGGCAGATGGAATG 780
737 CCAGCGACCCCTATGGTCAATGAGGACTGTGGAGATCCTGAGCTCTGGCAGATGGAATG 796
781 ACACAGAGTGGCATCTTACCATGTAATGCTGTGCTGTGAGTTCATCAGAGGAAAGTAAC 840
797 ACACAGAGTGGCATCTTACCATGTAATGCTGTGCTGTGAGTTCATCAGAGGAAAGTAAC 856
841 TTCCCTCATCTCAGTATTTGCTATTTTCTGTGTGACCGTCAATTACAGTATTGTTATCCA 900
857 TTCCCTCATCTCAGTATTTGCTATTTTCTGTGTGACCGTCAATTACAGTATTGTTATCCA 916
901 TCTTTTTTTTCTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 960
917 TCTTTTTTTTCTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 976
961 CTGAGGTATGGAGCTCCCATCATCA 985
977 CTGAGGTATGGAGCTCCCATCATCA 1001

RESULT 4
AS45974
D AAS45974 standard; cDNA; 1016 BP.
X C AAS45974;
X T 18-DEC-2001 (first entry)
X E Human DNA encoding PRO polypeptide sequence #50.
X W PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
W dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
W blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
W adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
W PCR primer.
X S Homo sapiens.
X N WO2001:68848-A2.
X D 20-SEP-2001.
X F 28-FEB-2001; 2001WO-US006520.
X R 01-MAR-2000; 2000WO-US005601.
R 02-MAR-2000; 2000WO-US005841.
R 03-MAR-2000; 2000US-0187202P.
R 06-MAR-2000; 2000US-0186968P.
R 14-MAR-2000; 2000US-0189320P.
R 14-MAR-2000; 2000US-0189328P.
R 15-MAR-2000; 2000WO-US006884.
R 21-MAR-2000; 2000US-0190828P.
R 21-MAR-2000; 2000US-0191007P.
R 21-MAR-2000; 2000US-0191048P.
R 21-MAR-2000; 2000US-0191314P.
R 28-MAR-2000; 2000US-0192855P.
R 29-MAR-2000; 2000US-0193032P.
R 29-MAR-2000; 2000US-0193053P.
R 30-MAR-2000; 2000WO-US008439.
R 04-APR-2000; 2000US-0194449P.
R 04-APR-2000; 2000US-0194647P.
R 11-APR-2000; 2000US-0195975P.
R 11-APR-2000; 2000US-0196000P.
R 11-APR-2000; 2000US-0196187P.

PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX (GETH) GENENTECH INC.
PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
P-PSDB; AAU29073.
XX WPI: 2001-602746/68.
XX P-PSDB; AAU29073.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 2; Fig 99; 774pp; English.
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
Query Match 61.5%; Score 980.2; DB 4; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.1e-279;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAATGAATGGCTTTTCGATCTCTGCTTCGCAAGAACCAATTTATCTCTGCTATAT 60
DB 17 CAGCAATGAATGGCTTTTCGATCTCTGCTTCGCAAGAACCAATTTATCTCTGCTATAT 76
QY 61 TTCTTTTGCATATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCT 120
DB 77 TTCTTTTGCATATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCT 136
QY 121 GTGCCACACACAAATTTCCACGAGACCCCAAGAGATGATGGTGAAGAGGATCCAG 180
DB 137 GTGCCACACACAAATTTCCACGAGACCCCAAGAGATGATGGTGAAGAGGATCCAG 196
QY 181 GAGAGAGGAGGAGGATGCGCAAGTGGCAGCCGATGGGCGCCGAAAGGAATTAAGAGAAC 240
DB 197 GAGAGAGGAGGAGGATGCGCAAGTGGCAGCCGATGGGCGCCGAAAGGAATTAAGAGAAC 256

PR	09-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088738P.	PR	13-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100664P.
PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088826P.	PR	16-SEP-1998;	98US-0101751P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088867P.	PR	17-SEP-1998;	98US-0100919P.
PR	12-JUN-1998;	98US-0088909P.	PR	17-SEP-1998;	98US-0100930P.
PR	12-JUN-1998;	98US-0089105P.	PR	18-SEP-1998;	98US-0100849P.
PR	16-JUN-1998;	98US-0089512P.	PR	18-SEP-1998;	98US-0101014P.
PR	16-JUN-1998;	98US-0089514P.	PR	18-SEP-1998;	98US-0101068P.
PR	17-JUN-1998;	98US-0089538P.	PR	23-SEP-1998;	98US-0101471P.
PR	17-JUN-1998;	98US-0089588P.	PR	23-SEP-1998;	98US-0101472P.
PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089608P.	PR	23-SEP-1998;	98US-0101477P.
PR	19-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101738P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101739P.
PR	22-JUN-1998;	98US-0090252P.	PR	24-SEP-1998;	98US-0101743P.
PR	22-JUN-1998;	98US-0090254P.	PR	24-SEP-1998;	98US-0101922P.
PR	24-JUN-1998;	98US-0090429P.	PR	24-SEP-1998;	98US-0101786P.
PR	24-JUN-1998;	98US-0090435P.	PR	23-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090444P.	PR	23-SEP-1998;	98US-0102240P.
PR	24-JUN-1998;	98US-0090461P.	PR	23-SEP-1998;	98US-0102330P.
PR	24-JUN-1998;	98US-0090535P.	PR	23-SEP-1998;	98US-0102331P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102487P.
PR	24-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090678P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090690P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090694P.	PR	01-OCT-1998;	98US-0102965P.
PR	25-JUN-1998;	98US-0090695P.	PR	06-OCT-1998;	98US-0103258P.
PR	25-JUN-1998;	98US-0090696P.	PR	06-OCT-1998;	98US-0103449P.
PR	26-JUN-1998;	98US-0090891P.	PR	07-OCT-1998;	98US-0016897B.
PR	26-JUN-1998;	98US-0090892P.			
PR	26-JUN-1998;	98US-0090863P.			
PR	26-JUN-1998;	98US-0091010P.			
PR	01-JUL-1998;	98US-0091359P.			
PR	02-JUL-1998;	98US-0091544P.			
PR	02-JUL-1998;	98US-0091478P.			
PR	02-JUL-1998;	98US-0091486P.			
PR	02-JUL-1998;	98US-0091626P.			
PR	02-JUL-1998;	98US-0091628P.			
PR	02-JUL-1998;	98US-0091832P.			
PR	02-JUL-1998;	98US-0094006P.			
PR	04-AUG-1998;	98US-0095282P.			
PR	10-AUG-1998;	98US-0095998P.			
PR	10-AUG-1998;	98US-0096012P.			
PR	17-AUG-1998;	98US-0096757P.			
PR	17-AUG-1998;	98US-0096766P.			
PR	17-AUG-1998;	98US-0096867P.			
PR	17-AUG-1998;	98US-0096891P.			
PR	17-AUG-1998;	98US-0096897P.			
PR	18-AUG-1998;	98US-0096949P.			
PR	18-AUG-1998;	98US-0096959P.			
PR	18-AUG-1998;	98US-0097022P.			
PR	26-AUG-1998;	98US-0097352P.			
PR	26-AUG-1998;	98US-0097354P.			
PR	26-AUG-1998;	98US-0097355P.			
PR	26-AUG-1998;	98US-0097371P.			
PR	26-AUG-1998;	98US-0097974P.			
PR	26-AUG-1998;	98US-0098014P.			
PR	01-SEP-1998;	98US-0098014P.			
PR	01-SEP-1998;	98US-0098716P.			
PR	01-SEP-1998;	98US-0098723P.			
PR	02-SEP-1998;	98US-0098803P.			
PR	02-SEP-1998;	98US-0098821P.			
PR	02-SEP-1998;	98US-0098843P.			
PR	09-SEP-1998;	98US-0099602P.			
PR	10-SEP-1998;	98US-0099741P.			
PR	10-SEP-1998;	98US-0099754P.			
Qy	1	CAGCAATGAATGGCTTTGCATCCTTGGCTTGGATATTTGATAGCGCTCCTACCGTGAAGTCT	60		
Db	17	CAGCAATGAATGGCTTTGCATCCTTGGCTTGGATATTTGATAGCGCTCCTACCGTGAAGTCT	76		
Qy	61	TTCTTTTGCATATTCAGAGTCTGGGTCTGGATATTTGATAGCGCTCCTACCGTGAAGTCT	120		
Db	77	TTCTTTTGCATATTCAGAGTCTGGGTCTGGATATTTGATAGCGCTCCTACCGTGAAGTCT	136		
Qy	121	GTGCCACACACACAATTTCCAGCAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAG	180		
Db	137	GTGCCACACACACAATTTCCAGCAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAG	196		
Qy	181	GAGAGAGGGAAGCATGGCAAGTGGGACCGCATGGGCCCAGAAAGGAATTAAGAGAAC	240		
Db	197	GAGAGAGGGAAGCATGGCAAGTGGGACCGCATGGGCCCAGAAAGGAATTAAGAGAAC	256		
Qy	241	TGGGTGATATGGAGATCGGGCAATATTTGGCAAGTGGGCCCAGAAAGGAATTAAGAGAAC	300		
Db	257	TGGGTGATATGGAGATCGGGCAATATTTGGCAAGTGGGCCCAGAAAGGAATTAAGAGAAC	316		
Qy	301	ACAAAGGGAAGGTTTGGTTCGATACCTGGAGAAAAGGCAAGGAGGAGTCTGCT	360		
Db	317	ACAAAGGGAAGGTTTGGTTCGATACCTGGAGAAAAGGCAAGGAGGAGTCTGCT	376		
Qy	361	GTGATTTGGAAGATACCGGAATTTGGTTCGATACCTGGAGAAAAGGCAAGGAGTCTGCT	420		
Db	377	GTGATTTGGAAGATACCGGAATTTGGTTCGATACCTGGAGAAAAGGCAAGGAGTCTGCT	436		
Qy	421	AGACATCTATGAAGTTTGTCAAGATTTGATAGCAGGAGTATGGGAAACTGAAGAGAAAT	480		
Db	437	AGACATCTATGAAGTTTGTCAAGATTTGATAGCAGGAGTATGGGAAACTGAAGAGAAAT	496		

Query Match 51.5%; Score 980.2; DB 7; Length 1016;

Best Local Similarity 99.7%; Pred. No. 1.1e-279;

Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 481 TCTACTACATCGTCAGGAGAGAACTACAGGAATCCCTAACCCACTGCAGGATTC 540
Db 497 TCTACTACATCGTCAGGAGAGAACTACAGGAATCCCTAACCCACTGCAGGATTC 556
QY 541 GGGGTGGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATG 600
Db 557 GGGGTGGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATG 616
QY 601 TTGCCAAGAGTGGCTCTTTGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGAGGGAC 660
Db 617 TTGCCAAGAGTGGCTCTTTGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGAGGGAC 676
QY 661 AGTACATGTTTCACAGACACACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 720
Db 677 AGTACATGTTTCACAGACACACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 736
QY 721 CCAGCGACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 780
Db 737 CCAGCGACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 796
QY 781 ACACAGAGTGCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAAGTAAC 840
Db 797 ACACAGAGTGCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAAGTAAC 856
QY 841 TTCCCTCATCTACGATTTGCTATTTTCTGTGACCGTCACTACATGATGATTTGTTATCCA 900
Db 857 TTCCCTCATCTACGATTTGCTATTTTCTGTGACCGTCACTACATGATGATTTGTTATCCA 916
QY 901 TCTTTTTTCTGATTTGATCTACATTTGATCTGATCTCAACATAGTAAATGCTTAAA 960
Db 917 TCTTTTTTCTGATTTGATCTACATTTGATCTGATCTCAACATAGTAAATGCTTAAA 976
QY 961 CTGAGTATGAGGCTTCATCATCA 985
Db 977 CTGAGTATGAGGCTTCATCATCA 1001

RESULT 6
ACA75549
ID ACA75549 standard; cDNA; 1016 BP.
AC ACA75549;
XX
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO702 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003032127-A1.
XX
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063122P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
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PR 18-MAY-1998; 98US-0086023P.
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PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
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PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.

R	16-JUN-1998;	98US-0089514P.	PR	23-SEP-1998;	98US-0101471P.	Query Match	61.5%;	Score 980.2;	DB 7;	Length 1016;
R	17-JUN-1998;	98US-0089538P.	PR	23-SEP-1998;	98US-0101472P.	Best Local Similarity	99.7%;	Pred. No. 1.e-279;		
R	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101475P.	Matches	982;	Conservative	0;	Mismatches 3;
R	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101477P.					Indels 0;
R	18-JUN-1998;	98US-0089908P.	PR	24-SEP-1998;	98US-0101738P.					Gaps 0;
R	19-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101739P.	QY	1	CAGCAATGAATGGCTTTGCATCCTTGGTTCGAGAAACCAATTTATCCTCTCGGTACTAT	60	
R	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101743P.	DB	17	CAGCAATGAATGGCTTTGCATCCTTGGTTCGAGAAACCAATTTATCCTCTCGGTACTAT	76	
R	22-JUN-1998;	98US-0090252P.	PR	24-SEP-1998;	98US-0101922P.	QY	61	TTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTCAAGTCT	120	
R	22-JUN-1998;	98US-0090254P.	PR	24-SEP-1998;	98US-0101922P.	DB	77	TTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTCAAGTCT	136	
R	24-JUN-1998;	98US-0090429P.	PR	25-SEP-1998;	98US-0101786P.	QY	121	GTGCCACACACACAAATTCACAGGATCCCAAGAGATGATGTTGATAGCGCTCCTACCGCTCAAGTCT	180	
R	24-JUN-1998;	98US-0090435P.	PR	25-SEP-1998;	98US-0102207P.	DB	137	GTGCCACACACACAAATTCACAGGATCCCAAGAGATGATGTTGATAGCGCTCCTACCGCTCAAGTCT	196	
R	24-JUN-1998;	98US-0090444P.	PR	25-SEP-1998;	98US-0102240P.	QY	181	GAGAAGAGGAAAGCATGGCAAGTGGGAGCGCATGGGCGCGAAAGGAAATTTAAAGGAGAAC	240	
R	24-JUN-1998;	98US-0090461P.	PR	25-SEP-1998;	98US-0102330P.	DB	197	GAGAAGAGGAAAGCATGGCAAGTGGGAGCGCATGGGCGCGAAAGGAAATTTAAAGGAGAAC	256	
R	24-JUN-1998;	98US-0090535P.	PR	29-SEP-1998;	98US-0102331P.	QY	241	TGGGTGATATGGGAGATCGGGCAATATTGGCAAGATCGGGCCCATTTGGGAAGAAGGGTG	300	
R	24-JUN-1998;	98US-0090540P.	PR	29-SEP-1998;	98US-0102487P.	DB	257	TGGGTGATATGGGAGATCGGGCAATATTGGCAAGATCGGGCCCATTTGGGAAGAAGGGTG	316	
R	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102570P.	QY	301	ACAAAGGGGAAAGGTTTGTCTGGATACCTGGAGAAAGGCAAGCAGGACTGTCT	360	
R	25-JUN-1998;	98US-0090678P.	PR	30-SEP-1998;	98US-0102571P.	DB	317	ACAAAGGGGAAAGGTTTGTCTGGATACCTGGAGAAAGGCAAGCAGGACTGTCT	376	
R	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102684P.	QY	361	GTGATTGTGGAAGTACCGGAAATTTGTGGACAACTGGATATTAGTATTGCCCGGTCA	420	
R	25-JUN-1998;	98US-0090690P.	PR	02-OCT-1998;	98US-0102687P.	DB	377	GTGATTGTGGAAGTACCGGAAATTTGTGGACAACTGGATATTAGTATTGCCCGGTCA	436	
R	25-JUN-1998;	98US-0090694P.	PR	06-OCT-1998;	98US-0102965P.	QY	421	AGACATCTATGAAGTTTGTCAAGATCTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT	480	
R	25-JUN-1998;	98US-0090695P.	PR			DB	437	AGACATCTATGAAGTTTGTCAAGATCTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT	496	
R	25-JUN-1998;	98US-0090696P.	PR			QY	481	TCTACTACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC	540	
R	25-JUN-1998;	98US-0090696P.	PR			DB	497	TCTACTACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC	556	
R	25-JUN-1998;	98US-0090696P.	PR			QY	541	GGGTTGGAATGCTAGCCATGCCAAGGATGAGCTGCCAACACACTCATCGTACTATG	600	
R	25-JUN-1998;	98US-0090696P.	PR			DB	557	GGGTTGGAATGCTAGCCATGCCAAGGATGAGCTGCCAACACACTCATCGTACTATG	616	
R	25-JUN-1998;	98US-0090696P.	PR			QY	601	TTGCCAAGAGTGGCTTCTTTTCGGGTGTTTTCATTGGCGTGAATGACCTTTGAAAGGAGGAGAC	660	
R	25-JUN-1998;	98US-0090696P.	PR			DB	617	TTGCCAAGAGTGGCTTCTTTTCGGGTGTTTTCATTGGCGTGAATGACCTTTGAAAGGAGGAGAC	676	
R	25-JUN-1998;	98US-0090696P.	PR			QY	661	AGTACATGTTCCAGACAACTCCACTCGTCAAGTCTAGCAACTGAAATGAGGGGAGAC	720	
R	25-JUN-1998;	98US-0090696P.	PR			DB	677	AGTACATGTTCCAGACAACTCCACTCGTCAAGTCTAGCAACTGAAATGAGGGGAGAC	736	

Qy	721	CCAGGACCCCTATGCTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG	780	PR	01-APR-1998;	98US-0080327P.
Db	737	CCAGGACCCCTATGCTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG	796	PR	01-APR-1998;	98US-0080333P.
2y	751	ACACAGAGTGCCATCTTACCATGACTTTGCTGTGAGATTTCATCAAGAAGAAAAGTAAC	840	PR	08-APR-1998;	98US-0081049P.
Db	797	ACACAGAGTGCCATCTTACCATGACTTTGCTGTGAGATTTCATCAAGAAGAAAAGTAAC	856	PR	09-APR-1998;	98US-0081195P.
2y	841	TTCCCTCATCTTACGATTTGCTATTTTCCTGTGACCGTCAATACAGTTATTTGTTATCCA	900	PR	15-APR-1998;	98US-0081838P.
Db	857	TTCCCTCATCTTACGATTTGCTATTTTCCTGTGACCGTCAATACAGTTATTTGTTATCCA	916	PR	21-APR-1998;	98US-0082568P.
2y	901	TCCTTTTTCCTGATTGTACTACATTTGATCTGAGTCAACATAGTCAGAAAATGCTAAA	960	PR	21-APR-1998;	98US-0082569P.
Db	917	TCCTTTTTCCTGATTGTACTACATTTGATCTGAGTCAACATAGTCAGAAAATGCTAAA	976	PR	22-APR-1998;	98US-0082704P.
2y	961	CTGAGGTATGAGCGCTCCATCATCA 985		PR	22-APR-1998;	98US-0082797P.
Db	977	CTGAGGTATGAGCGCTCCATCATCA 1001		PR	28-APR-1998;	98US-0083322P.
RESULT 7						98US-0083495P.
ID	ACA71029 standard; cDNA; 1016 BP.					98US-0083496P.
AC	ACA71029;					98US-0083559P.
DT	02-AUG-2003 (first entry)					98US-0084366P.
DE	Human secreted/transmembrane protein (PRO) cDNA #50.					98US-0084414P.
KW	Human; Gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;					98US-0084639P.
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;					98US-0084643P.
KW	tissue typing.					98US-0085579P.
OS	Homo sapiens.					98US-0085580P.
OS	US2003032112-A1.					98US-0085582P.
PN	13-FEB-2003.					98US-0085700P.
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PR	21-NOV-1997; 97US-0065311P.					98US-0088202P.
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PR	17-DEC-1997; 97US-0069425P.					98US-0088262P.
PR	18-DEC-1997; 97US-0069870P.					98US-0088611P.
PR	10-MAR-1998; 97US-0068017P.					98US-0088624P.
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R 23-SEP-1998; 98US-0102331P.
R 30-SEP-1998; 98US-0102487P.
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PR 02-OCT-1998; 98US-0102965P.
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PR 07-OCT-1998; 98US-00168978.

Query Match 61.5%; Score 980.2; DB 7; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.1e-279;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 TTTCTTTTGCATAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTACCGCTGAAGTCT 120
DB 77 TTTCTTTTGCATAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTACCGCTGAAGTCT 136
QY 121 GTGCCACACACACAATTTTCACAGGACCCCAAGAGATGATGTGAAAAAGGAGATCCAG 180
DB 137 GTGCCACACACACAATTTTCACAGGACCCCAAGAGATGATGTGAAAAAGGAGATCCAG 196
QY 181 GAGAGAGGGAAGCAGTGGCAAGTGGAGCGCATGGGCGCGAAGGAATTTAAAGGAGAAC 240
DB 197 GAGAGAGGGAAGCAGTGGCAAGTGGAGCGCATGGGCGCGAAGGAATTTAAAGGAGAAC 256
QY 241 TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGGCCCATTTGGGAAGAGGGTG 300
DB 257 TGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGGCCCATTTGGGAAGAGGGTG 316
QY 301 ACAAGGGGAAAAAGTTTGTCTGGATATCTGGAGAAAAAGGCAAGCAGGTACTGTCT 360
DB 317 ACAAGGGGAAAAAGTTTGTCTGGATATCTGGAGAAAAAGGCAAGCAGGTACTGTCT 376
QY 361 GTGATTGTGGAAGTACCGGAAATTTCTTGGCAACTTGGATATTAGTATTGCCGGGTCA 420
DB 377 GTGATTGTGGAAGTACCGGAAATTTCTTGGCAACTTGGATATTAGTATTGCCGGGTCA 436
QY 421 AGACATCTATGAAGTTTGTCAAGATGTGATAGCGGATTAGGGAACCTGAAGAGAAAT 480
DB 437 AGACATCTATGAAGTTTGTCAAGATGTGATAGCGGATTAGGGAACCTGAAGAGAAAT 496
QY 481 TCTACTACATCGTCAGAGAGAGAAAGTACAGGGAATCCCTAACCCACTGCAGAGATTC 540
DB 497 TCTACTACATCGTCAGAGAGAGAGAAAGTACAGGGAATCCCTAACCCACTGCAGAGATTC 556
QY 541 GGGGTGGAATCTAGCCATGCCAAGGATGAAGTGCACACACTCATGCTGACTATG 600
DB 557 GGGGTGGAATCTAGCCATGCCAAGGATGAAGTGCACACACTCATGCTGACTATG 616
QY 601 TTGCCAAGTGGCTTCTTTGGGTGTTTCAATGGCGTGAATGACCTTGAAGGGAGGAC 660
DB 617 TTGCCAAGTGGCTTCTTTGGGTGTTTCAATGGCGTGAATGACCTTGAAGGGAGGAC 676
QY 661 AGTACATGTTACAGACACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 720
DB 677 AGTACATGTTACAGACACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 736
QY 721 CCAGGACCCCTATGTCATGAGGACTGTCTGGAGTGTGAGCTCTGGCAGATGGAATG 780
DB 737 CCAGGACCCCTATGTCATGAGGACTGTCTGGAGTGTGAGCTCTGGCAGATGGAATG 796
QY 781 ACACAGAGTGCATCTTACCATGTACTTTTGTCTGTGAGTTTCATCAAGAGAAAAAGTAAC 840
DB 797 ACACAGAGTGCATCTTACCATGTACTTTTGTCTGTGAGTTTCATCAAGAGAAAAAGTAAC 856
QY 841 TTCCCTCATCTAGTATTGCTATTTTCTGTGACCGTCAATTACAGTTATTGTTATCCA 900
DB 857 TTCCCTCATCTAGTATTGCTATTTTCTGTGACCGTCAATTACAGTTATTGTTATCCA 916
QY 901 TCCCTTTTCTGATGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAAA 960
DB 917 TCCCTTTTCTGATGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAAA 976

QY 961 CTGAGGTATGAGCCTCATCATCA 985
Db 977 CTGAGGTATGAGCCTCATCATCA 1001

RESULT 8
ACC87557
ID ACC87557 standard; cDNA; 1016 BP.
AC ACC87557;
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JT 05-AUG-2003 (first entry)
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DE Human secreted polypeptide PRO702-encoding cDNA, SEQ ID NO:99.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.
DS Homo sapiens.
XX
PN US2003027278-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
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PR 24-NOV-1997; 97US-0066466P.
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PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
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PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
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PR 01-APR-1998; 98US-0080333P.
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PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
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PR 28-APR-1998; 98US-0083322P.
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R	R	04-AUG-1998;	98US-0094006P.	
R	R	04-AUG-1998;	98US-0095282P.	
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R	R	10-AUG-1998;	98US-0096012P.	
R	R	17-AUG-1998;	98US-0096757P.	
R	R	17-AUG-1998;	98US-0096766P.	
R	R	17-AUG-1998;	98US-0096867P.	
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R	R	17-AUG-1998;	98US-0096897P.	
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R	R	26-AUG-1998;	98US-0097952P.	
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R	R	26-AUG-1998;	98US-0097955P.	
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R	R	26-AUG-1998;	98US-0097974P.	
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R	R	16-SEP-1998;	98US-0101751P.	
R	R	16-SEP-1998;	98US-01019330.	
R	R	17-SEP-1998;	98US-0100683P.	
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R	R	17-SEP-1998;	98US-0100930P.	
R	R	18-SEP-1998;	98US-0100849P.	
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R	R	18-SEP-1998;	98US-0101068P.	
R	R	23-SEP-1998;	98US-0101471P.	
R	R	23-SEP-1998;	98US-0101472P.	
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R	R	25-SEP-1998;	98US-0101786P.	
R	R	29-SEP-1998;	98US-0102207P.	
R	R	29-SEP-1998;	98US-0102240P.	
R	R	29-SEP-1998;	98US-0102330P.	
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R	R	30-SEP-1998;	98US-0102487P.	
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R	R	30-SEP-1998;	98US-0102571P.	
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Query Match 61.5%; Score 980.2; DB 7; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.1e-279;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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b	17	CAGCAATGAATGCTTTGGATCTCTGCTTCGAGAAACCAATTTATCTCTCTGCTACTAT	76
Y	61	TTCTTTTGCAGAAATTCAGAGTCTGGGCTCTGGATATTGATAGCGCTCTACCGCTGAAGTCT	120
b	77	TTCTTTTGCAGAAATTCAGAGTCTGGGCTCTGGATATTGATAGCGCTCTACCGCTGAAGTCT	136

QY	121	GTGCCACACACACAAATTTCCACGAGACCCAAAGGAGATGATGGTGAATAAAGGAGATCCAG	180
DB	137	GTGCCACACACACAAATTTCCACGAGACCCAAAGGAGATGATGGTGAATAAAGGAGATCCAG	196
QY	181	GAGAAAGAGGAAAGCATGGCAAAAGTGGGACCCATGGGCCCCGAAAGGAAATTAAGAGAGAAC	240
DB	197	GAGAAAGAGGAAAGCATGGCAAAAGTGGGACCCATGGGCCCCGAAAGGAAATTAAGAGAGAAC	256
QY	241	TGGGTGATATGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAAGAGGTTG	300
DB	257	TGGGTGATATGGAGATCAGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAAGAGGTTG	316
QY	301	ACAAAGGGGAAAGAGTTCCTTGGATACCTCGAGAAAAGGCAAAAGGCAAGCAGTACTCTCT	360
DB	317	ACAAAGGGGAAAGAGTTCCTTGGATACCTCGAGAAAAGGCAAAAGGCAAGCAGTACTCTCT	376
QY	361	GTGATTGTGGAAGATACCGGAAATTTGTTGGCAACTTTGGCAACTTTAGTATTAGTCCCGGTCA	420
DB	377	GTGATTGTGGAAGATACCGGAAATTTGTTGGCAACTTTAGTATTAGTATTAGTCCCGGTCA	436
QY	421	AGACATCTATGAAGTTCTCAAGAAATGTAGCAGGATTTAGGGAACCTGAAGAGAAAT	480
DB	437	AGACATCTATGAAGTTCTCAAGAAATGTAGCAGGATTTAGGGAACCTGAAGAGAAAT	496
QY	481	TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC	540
DB	497	TCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC	556
QY	541	GGGTTGGAATGCTACCCATGCCAGGATGAAGTGCACACACTCATCGTCACTATG	600
DB	557	GGGTTGGAATGCTACCCATGCCAGGATGAAGTGCACACACTCATCGTCACTATG	616
QY	601	TTGCCAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGAGGAGGAC	660
DB	617	TTGCCAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGAGGAGGAC	676
QY	661	AGTACATGTTACAGACAACTCCACTGCGAGACTATAGCAACTGGAATGAGGGGAAAC	720
DB	677	AGTACATGTTACAGACAACTCCACTGCGAGACTATAGCAACTGGAATGAGGGGAAAC	736
QY	721	CCAGCGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG	780
DB	737	CCAGCGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG	796
QY	781	ACACAGAGTGCCATCTTACCATGTTCTTGTGTGAGTTTCATCAAGAGAAAGTAAC	840
DB	797	ACACAGAGTGCCATCTTACCATGTTCTTGTGTGAGTTTCATCAAGAGAAAGTAAC	856
QY	841	TTCCCTCATCTTACGTTATTTGCTATTTCTGTCGACCGTCAATTACAGTTATTGTTATCCA	900
DB	857	TTCCCTCATCTTACGTTATTTGCTATTTCTGTCGACCGTCAATTACAGTTATTGTTATCCA	916
QY	901	TCCTTTTTCCTGATGTTACTATGATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA	960
DB	917	TCCTTTTTCCTGATGTTACTATGATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA	976
QY	961	CTGAGGTATGGAGCCTCCATCATCA	985
DB	977	CTGAGGTATGGAGCCTCCATCATCA	1001

RESULT 9
ACC86943
ID ACC86943 standard; cDNA; 1016 BP.
XX ACC86943;
AC ACC86943;
XX DT 05-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO702-encoding cDNA, SEQ ID NO:99.
XX KW Human; PRO; secreted protein; transmembrane protein;

KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.
OS Homo sapiens.
FX XX
FX US2003036159-A1.
XX XX
XX 20-FEB-2003.
XX XX
XX 02-JUL-2002; 2002US-00188773.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.
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XX 18-DEC-1997; 97US-0068017P.
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24-SEP-1998;	98US-0101743P.	PR
25-SEP-1998;	98US-0101922P.	PR
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29-SEP-1998;	98US-0102240P.	PR
29-SEP-1998;	98US-0102330P.	PR
29-SEP-1998;	98US-0102331P.	PR
30-SEP-1998;	98US-0102487P.	PR
30-SEP-1998;	98US-0102570P.	PR
30-SEP-1998;	98US-0102571P.	PR
01-OCT-1998;	98US-0102684P.	PR
01-OCT-1998;	98US-0102687P.	PR
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Best Local Similarity 99.7%; Pred. No. 1.1e-279;		
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
1	CAGCAATGAATGGCTTGCATCCCTTCGTCGAGAAACCAATTTATCCTCTGGTACTAT 60	
17	CAGCAATGAATGGCTTGCATCCCTTCGTCGAGAAACCAATTTATCCTCTGGTACTAT 76	
61	TTCTTTTTCGCAATTCAGAGTCTGGGCTCGATATTGATAGCGCTCCTACCGCTGAAGTCT 120	
77	TTCTTTTTCGCAATTCAGAGTCTGGGCTCGATATTGATAGCGCTCCTACCGCTGAAGTCT 136	
121	GTGCCACACACAATTTCCACAGGACCCAAAGAGAGATGATCGTCAAAAAGAGATCCAG 180	
137	GTGCCACACACAATTTCCACAGGACCCAAAGAGAGATGATCGTCAAAAAGAGATCCAG 196	
181	GAGAAGAGGGAAGAGCATGGCAAGTGGAGCGCATGGGCGCGCAAGGAATTAAGAGAGAC 240	
197	GAGAAGAGGGAAGAGCATGGCAAGTGGAGCGCATGGGCGCGCAAGGAATTAAGAGAGAC 256	
241	TGGGTGATATGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 300	
257	TGGGTGATATGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 316	
301	ACAAAGGGGAAAAGGTTTCTTGGATACCTTGGAGAAAAGGCAAGCAGGTACTGTCT 360	
317	ACAAAGGGGAAAAGGTTTCTTGGATACCTTGGAGAAAAGGCAAGCAGGTACTGTCT 376	

Qy	361	GTGATTGTGGAAGATACCGGAAATTTGTTGGCAAACTGGATATTAGTATTCGCCGCTCA 420
Db	377	GTGATTGTGGAAGATACCGGAAATTTGTTGGCAAACTGGATATTAGTATTCGCCGCTCA 436
Qy	421	AGACATCTATGAAGTTTCTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAAT 480
Db	437	AGACATCTATGAAGTTTCTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAAT 496
Qy	481	TCTACTACATCTCGTCAGGAAGAAAGAACTACAGGGAATCCCTAACCCACTGCAGATTTC 540
Db	497	TCTACTACATCTCGTCAGGAAGAAAGAACTACAGGGAATCCCTAACCCACTGCAGATTTC 556
Qy	541	GGGGTGGAAATGTAGCCATGCCCAAGGATGAAGTCCCAACACTCATCGCTGACTATG 600
Db	557	GGGGTGGAAATGTAGCCATGCCCAAGGATGAAGTCCCAACACTCATCGCTGACTATG 616
Qy	601	TTGCCAAGAGTGGCTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGAC 660
Db	617	TTGCCAAGAGTGGCTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGAC 676
Qy	661	AGTACATGTTCAACAGAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 720
Db	677	AGTACATGTTCAACAGAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 736
Qy	721	CCAGCGACCCCTATGCTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 780
Db	737	CCAGCGACCCCTATGCTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 796
Qy	781	ACACAGAGTGGCATCTTACCATGTTACTTTGCTGTGAGTTTATCAAGAGAAAAGTAAC 840
Db	797	ACACAGAGTGGCATCTTACCATGTTACTTTGCTGTGAGTTTATCAAGAGAAAAGTAAC 856
Qy	841	TTCCCTCTCATCTACGATATTGCTATTTTCTGTGACCGCTCATTTACAGTTATTGTTATCCA 900
Db	857	TTCCCTCTCATCTACGATATTGCTATTTTCTGTGACCGCTCATTTACAGTTATTGTTATCCA 916
Qy	901	TCCTTTTTCCTGATGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA 960
Db	917	TCCTTTTTCCTGATGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA 976
Qy	961	CTGAGGTATGGAGCTCCCATCATCA 985
Db	977	CTGAGGTATGGAGCTCCCATCATCA 1001
RESULT 10		
ACD04116		
ID	ACD04116	standard; cDNA; 1016 BP.
XX	ACD04116;	
AC	ACD04116;	
XX	XX	
DT	09-AUG-2003	(first entry)
XX	XX	
DE	Human secreted/transmembrane protein (PRO) cDNA #50.	
XX	XX	
KW	Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;	
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	US2003040070-A1.	
XX	XX	
PD	27-FEB-2003.	
XX	XX	
PF	27-JUN-2002; 2002US-00184627.	
XX	XX	
PR	18-SEP-1997; 97US-0059263P.	
PR	18-SEP-1997; 97US-0059266P.	
PR	17-OCT-1997; 97US-0062250P.	
PR	21-OCT-1997; 97US-0063486P.	
PR	24-OCT-1997; 97US-0063120P.	

	17-SEP-1998;	98US-0100683P.	
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'R	17-SEP-1998;	98US-0100919P.	
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'R	23-SEP-1998;	98US-0101471P.	
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'R	01-OCT-1998;	98US-0102684P.	
'R	01-OCT-1998;	98US-0102687P.	
'R	02-OCT-1998;	98US-0102965P.	
'R	06-OCT-1998;	98US-0103258P.	
'R	06-OCT-1998;	98US-0103449P.	
'R	07-OCT-1998;	98US-0016897B.	
	Query Match	61.5%;	Score 980.2; DB 7; Length 1016;
	Best Local Similarity	99.7%;	Pred. No. 1.le-279;
	Matches 982;	Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
'Y	1	CAGCAATGAATGGCTTTGCATCCTTGCTTCGAAAGAAACCAATTATTCCTCGTACTCAT	60
'b	17	CAGCAATGAATGGCTTTGCATCCTTGCTTCGAAAGAAACCAATTATTCCTCGTACTCAT	76
'Y	61	TTCITTTTCCAAATTCAGAGTCTGGGTCTCGATATTGATAGCCGTCTCTACC GGCTGAAGTCT	120
'b	77	TTCITTTTCCAAATTCAGAGTCTGGGTCTCGATATTGATAGCCGTCTCTACC GGCTGAAGTCT	136
'Y	121	GTGCCACACACACAATTTCCACAGGACCCAAAGAGATGATGTGTAAGAAGAGATCCAG	180
'b	137	GTGCCACACACACAATTTCCACAGGACCCAAAGAGATGATGTGTAAGAAGAGATCCAG	196
'Y	181	GAGAAGAGGGAAACATGCGAAATGGGACGCGATGGCGCGAAGCGAAGAAATTAAGGAGAAC	240
'b	197	GAGAAGAGGGAAACATGCGAATGGGACGCGATGGCGCGAAGCGAAGAAATTAAGGAGAAC	256
'Y	241	TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCAATTGGGAAGAAGGGTG	300
'b	257	TGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCAATTGGGAAGAAGGGTG	316
'Y	301	ACAAAGGGGAAAAGGTTTGCCTGGATACCTGGAGAAAGCAAGCAAGTACTGTCT	360
'b	317	ACAAAGGGGAAAAGGTTTGCCTGGATACCTGGAGAAAPAGCAAGCAAGTACTGTCT	376
'Y	361	GTGATTTGGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCCCGGCTCA	420
'b	377	GTGATTTGGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCCCGCTCA	436
'Y	421	AGACATCTATGAAGTTTGTCAAGATGTGNATGACGGGATTAGGGAAACTGAAGAGAAAT	480
'b	437	AGACATCTATGAAGTTTGTCAAGATGTGNATGACGGGATTAGGGAAACTGAAGAGAAAT	496
'Y	481	TCTACTACATCGTCCAGGAAGAGAAATACTACAGGGAATCCCCTAACCCACTCCAGATTTC	540
'b	497	TCTACTACATCGTCCAGGAAGAGAGAACTACAGGGAATCCCCTAACCCACTCCAGATTTC	556
'Y	541	GGGTGGAAATGCTAGCCATGCCCAAGATGAAGCTGCCAACACATCATPCGCTGACTATG	600
'b	557	GGGTGGAAATGCTAGCCATGCCCAAGATGAAGCTGCCAACACATCATPCGCTGACTATG	616

Qy	601	TTGCCAAGAGTGGCTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTTGAAAGGGAGGGAC	666
Db	617	TTGCCAAGAGTGGCTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTTGAAAGGGAGGGAC	676
Qy	661	AGTACATGTTTCACAGACAACACTCCACTGCGAGAACTATAGCAACTGCAATGAGGGGGAAC	720
Db	677	AGTACATGTTCCACAGACAACACTCCACTGCGAGAACTATAGCAACTGCAATGAGGGGGAAC	736
Qy	721	CCAGCGACCCCTATGGTCATGAGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG	780
Db	737	CCAGCGACCCCTATGGTCATGAGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG	796
Qy	781	ACACAGAGTGGCCATCTTACCATGTACTTTGCTGCTGAGTTTCATCAAGAAAGAAAAGTAAC	840
Db	797	ACACAGAGTGGCCATCTTACCATGTACTTTGCTGCTGAGTTTCATCAAGAAAGAAAAGTAAC	856
Qy	841	TTCCCTCATCTTACGTATTTGCTATTTTCCTGTGACCCGTCAATTACAGTTATTGTTATCCA	900
Db	857	TTCCCTCATCTTACGTATTTGCTATTTTCCTGTGACCCGTCAATTACAGTTATTGTTATCCA	916
Qy	901	TCTTTTTCCTGATGCTACTACATTGTGCTGAGTCAACATAGCTAGAGAAATGCTAAA	960
Db	917	TCTTTTTCCTGATGCTACTACATTGTGCTGAGTCAACATAGCTAGAGAAATGCTAAA	976
Qy	961	CTGAGTATGGAGCCTCCATCATCA	985
Db	977	CTGAGTATGGAGCCTCCATCATCA	1001
RESULT 11			
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ID	ACA69447 standard; cDNA; 1016 BP.		
XX	ACA69447;		
AC	ACA69447;		
XX	27-JUN-2003 (first entry)		
DT	cDNA encoding human PRO polypeptide #50.		
XX	Human; PRO polypeptide; secreted and transmembrane protein; tumour;		
KW	chromosome mapping; gene mapping; cytosolic; gene therapy; gene; ss.		
XX	Homo sapiens.		
OS	US2003032113-A1.		
PN	13-FEB-2003.		
PD	20-JUN-2002; 2002US-00176911.		
XX	18-SEP-1997; 97US-0059263P.		
PR	18-SEP-1997; 97US-0059266P.		
PR	17-OCT-1997; 97US-0082250P.		
PR	21-OCT-1997; 97US-0083486P.		
PR	24-OCT-1997; 97US-0063120P.		
PR	24-OCT-1997; 97US-0063121P.		
PR	28-OCT-1997; 97US-0063540P.		
PR	28-OCT-1997; 97US-0063541P.		
PR	28-OCT-1997; 97US-0063544P.		
PR	28-OCT-1997; 97US-0083564P.		
PR	29-OCT-1997; 97US-0083573P.		
PR	31-OCT-1997; 97US-0063870P.		
PR	31-OCT-1997; 97US-0064103P.		
PR	13-NOV-1997; 97US-0065311P.		
PR	21-NOV-1997; 97US-0065120P.		
PR	24-NOV-1997; 97US-0066466P.		
PR	24-NOV-1997; 97US-0066772P.		
PR	11-DEC-1997; 97US-0089335P.		
PR	12-DEC-1997; 97US-0089425P.		
PR	17-DEC-1997; 97US-0068970P.		
PR	18-DEC-1997; 97US-0068017P.		
PR	10-MAR-1998; 98US-0077450P.		

PR	21-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0091010P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091359P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-0091544P.
PR	22-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-0091478P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091486P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091626P.
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PR	29-APR-1998;	98US-0083559P.	PR	02-JUL-1998;	98US-0091632P.
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PR	02-JUN-1998;	98US-0087650P.	PR	26-AUG-1998;	98US-0097955P.
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Query Match 61.5%; Score 980.2; DB 7; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.1e-279;

Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
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61	TTCTTTTGGCAATTCAGAGTCTGGTCTGGATATTGATAGCCGCTCTACCGCTGAGTCT	120	
77	TTCTTTTGGCAATTCAGAGTCTGGTCTGGATATTGATAGCCGCTCTACCGCTGAGTCT	136	
121	GTGCCACACACAAATTTACCAAGAGAGATGATGCTGAAAGAGAGATCCAG	180	
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181	GAGAGAGAGAGAGATGCGAAGAGTGGAGCGATGGGCGGAAAGAAATTAAGAGAAC	240	
197	GAGAGAGAGAGAGATGCGAAGAGTGGAGCGATGGGCGGAAAGAAATTAAGAGAAC	256	
241	TGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG	300	
257	TGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG	316	
301	ACAAAGGGGAAAAGGTTTCTTGGAAATACCTGGAGAAAGGCAAGAGGTA	360	
317	ACAAAGGGGAAAAGGTTTCTTGGAAATACCTGGAGAAAGGCAAGAGGTA	376	
361	GTGATTGTGGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTGCCGGCTCA	420	
377	GTGATTGTGGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTGCCGGCTCA	436	
421	AGACATCTATGAATTTGTCAAGAAATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT	480	
437	AGACATCTATGAATTTGTCAAGAAATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT	496	
481	TCTACTACATCGTCAGAGAGAGAACTACAGGAAATCCCTAACCCACTGCAGGATTC	540	
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541	GGGTGGAATGCTAGGCAATCCCAAGGATGAAGCTGCCAACACATCTCGTGTGATG	600	
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601	TTGCCAGAGTGGCTTTTCGGGTGTTCAATGGCGTGAATGACCTGAAAGGGAGGAC	660	
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661	AGTACATGTTCCACAGACACACCTCCACTGAGAACTATAGCAACTGGAATGAGGGGAAAC	720	
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721	CCAGGAGCCCTATGGTCATGAGGACTGTGTGAGATGCTGAGCTTGGCAGATGGAATG	780	
737	CCAGGAGCCCTATGGTCATGAGGACTGTGTGAGATGCTGAGCTTGGCAGATGGAATG	796	
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797	ACACAGAGTGCATCTTACCATGTTCTGTGAGTTCATCAAGAGAAAGAAAGTAAAC	856	
841	TTCCCTCATCTAGATTTGCTATTTCTGTGACCGCTCATTAAGTATTGTTATCA	900	
857	TTCCCTCATCTAGATTTGCTATTTCTGTGACCGCTCATTAAGTATTGTTATCA	916	
901	TCCCTTTTCTCATGTTACTACATTTGATCTGAGTCAACATAGTCAAAAATGCTAAA	960	
917	TCCCTTTTCTCATGTTACTACATTTGATCTGAGTCAACATAGTCAAAAATGCTAAA	976	
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977	CTGAGTATGAGGCTCCATCATCA	1001	

RESULT 13
ACC89399

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XX	
DT	11-AUG-2003 (first entry)
XX	
DE	Human secreted polypeptide PRO702-encoding cDNA, SEQ ID NO:99.
XX	
KW	Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnery; gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2003027264-A1.
XX	
PD	06-FEB-2003.
XX	
PF	18-JUN-2002; 2002US-00174579.
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PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 61.5%; Score 980.2; DB 7; Length 1016;
Best Local Similarity 99.7%; Pred. No. 1.1e-279;
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QY 61 TTTCTTTTGCATTAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTTACCGCTGAAGTCT 120
DB 77 TTTCTTTTGCATTAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTTACCGCTGAAGTCT 136
QY 121 GTGCCACACACACAATTTACCAGACCCAAAGAGATGATGTGAAAGAGGATCCAG 190
DB 137 GTGCCACACACACAATTTACCAGACCCAAAGAGATGATGTGAAAGAGGATCCAG 196
QY 181 GAGAAAGAGGAAAGCATGGCAAAAGTGGGACGCATGGGGCCGAAAGGAATTTAAAGGAGAAC 240

197 GAGAAAGGGAAGCATGGCAAGTGGACGCGATGGGCGCGAAGGAATTAAGGAGAAC 256
241 TGGGTGATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGCGGTG 300
257 TGGGTGATATGGGAGATCAGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGCGGTG 316
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317 ACAAGGGGAAAAGGTTTCTTTGGATACCTGGAGAAAAGGCAAGCAGGTACTGTCT 376
361 GTGATTTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTTGCCCGCTCA 420
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781 ACAGAGTGGCATCTTACCATGCTACTTTCTGTGAGTTCATCAAGAGAAAAGTAAC 840
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841 TTCCCTCATCTAGGATTTGCTATTTCTGTGAGCCGTCATCAGTATTTGTTATCCA 900
857 TTCCCTCATCTAGGATTTGCTATTTCTGTGAGCCGTCATCAGTATTTGTTATCCA 916
901 TCCTTTTTCCTGATGTACTACTATTTGATCTGAGTCAACATAGTGAATAATGCTAAA 960
917 TCCTTTTTCCTGATGTACTACTATTTGATCTGAGTCAACATAGTGAATAATGCTAAA 976
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RESULT 14

CA98190
D ACA98190 standard; cDNA; 1016 BP.

C ACA98190;

X ACA98190;

25-JUL-2003 (first entry)

Novel human secreted and transmembrane protein PRO702 cDNA.

Human; secreted and transmembrane protein; PRO; transgenic animal;
knockout; chromosome identification; tissue typing; tumour;
chondrocyte proliferation; chondrocyte differentiation;
tumour necrosis factor-alpha release stimulator; gene; ss.

NS Homo sapiens.

X US2003036144-A1.

XX 20-FEB-2003.
PD 01-JUL-2002; 2002US-00187601.
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XX 97US-0062250P.
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XX DT 18-JUL-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) cDNA #50.
XX KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
XX KW proliferation; differentiation; chondrocyte cell; TNF-alpha;
XX KW tumour necrosis factor-alpha; gene therapy.
XX OS Homo sapiens.
XX PN US2003036149-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00187746.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS	TITLE
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JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Db 181 GAGGAAAGCAATGGCAAGTGGGACGCTGGGGCGAAAGCAATTAAGGAGAACTGGGT 240
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QY 726 GACCCCTATGGTCTCAGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 785
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QY 786 GAGTGCCATCTTACCATGTACTTTGTCTGTAGTTTCATCAAGAGAAAGAAAGTAA 839
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DEFINITION Pan troglodytes COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY409411
VERSION AY409411.1 GI:39765379
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
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Best Local Similarity 99.4%; Pred. No. 8.4e-214;
Matches 829; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 66 TTGCAAAATTCAGAGTCTGGGTCTGGATATTCATAGCCGCTCTACCGCTGAAGTCTGTGCC 125
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QY 186 GAGGAAAGCAATGGCAAGTGGGACGCTGGGGCGAAAGCAATTAAGGAGAACTGGGT 245
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QY 246 GATATCGGAGATCGGGCAATTTTGGCAAACTGGGCTTGTGGTCTGCTGCTGCTGCTG 305
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QY 366 TGTGGAAGATACCGGAAATTTTGTGGCAAACTGGGATATTAGTATTTGCCCGCTCAAGACA 425

Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 4591)
TITLE
JOURNAL
REFERENCE
AUTHORS
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akanaha, S.,
 Takeda, Y., Tanaka, T., Tonari, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 Location/Qualifiers
 1. 4591
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FEATURES

source

CDS

ORIGIN

Query Match 42.4%; Score 675.8; DB 11; Length 4591;
 Best Local Similarity 83.1%; Pred. No. 1.4e-172;
 Matches 782; Conservative 0; Mismatches 157; Indels 2; Gaps 1;
 2 AGCAATGAATGGCTTCATCCTTGGTTCGAGAAACCAATTAATCCTCTGGTACTATT 61
 3 AGTCATGAATGGCTTTAGATCTCTGCTTCGAGCAACCTATCCTGCTGTGGCTAGC 62
 62 TCTTTTGCATATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCCTACCGCTGAAGTCTG 121
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QY 122 TGCACACACACATTTTCACAGGACCCCAAGGAGATGATGTGAAAAAGGAGATCCAGG 181
 Db 123 TGCACACACATACCATTTTCACAGGACCTAAAGGGGATGATGTGAAAGAGGTGACACAGG 182
 QY 182 AGAAGAGGGGAAACCATGCGCAAGTGGGAGCGCATTGGGCGCGGAAAGGAATTAAGAGGAGAACT 241
 Db 183 AGAAGAGGCGCAAGGATGGCAAGTGGGACCGCAGGAGACCAGAAAGGAGTGAAGAGGAGCT 242
 QY 242 GGGTGATATGGGAGATCGGGGCAATATTGGCAAGTATGGGCCCATTTGGCAAGAGGTTGA 301
 Db 243 GGGTGATATGGGAGCCAGGGTAAATTGGCAAGTCTGGCCCTATTGGCAAGAGGTTGA 302
 QY 302 CAAAGGGGAAAAAGGTTTGGTTGGAATACCTGGAGAAAAAGGCAAGCAGGCTACTGTTCTG 361
 Db 303 CAAAGGGGAAAAAGGTTCTGCTTGGATTTCTGGAGAAAAAGGCAAGCAGGCTACTGTTCTG 362
 QY 362 TGATTGTGGAGATACCGGAATTTGTTGGCAACACTGGATATTAGTATTGCTCCCGCTCAA 421
 Db 363 TGATTGTGGCAGGTACCGGAAGTGGTGGCAACACTGGATATTAGTATTGCTCCGCTCAA 422
 QY 422 GACATCTATGAAGTTTGTCAAGATGTAGTACGAGGATTTAGGGAACTTGAAGAGAAATT 481
 Db 423 GACATCAATGAATTTCAAGATGTATTAGCGGGATCCGGGAACTTGAAGAGAAATT 482
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 Db 483 CTACTACATGTCGAGGAGGAGAGAACTTACAGGGAATCTCTGACCCACTGCAGGATCCG 542
 QY 542 GGGTGAATGCTAGCCATGCCCAAGGATGAAGTCCCAACACACTCATCGCTGCTGACTATGT 601
 Db 543 AGGAGGATGCTAGCCATGCCCAAGGATGAAGTCCCAACACTCATCGCTGCTGACTATGT 602
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 QY 662 GTACATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGCGATGAGGGGAGACC 721
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 QY 782 CACAGAGTGCATTTACCATGCTATCTTGTCTGTGAGTTCATCAAGAGAAAGAAAGTAACT 841
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 QY 842 TCCCTCATCTACGTATTGCTATTTCCTGTGACCGCTCATTACAGTTATTGCTTATCCAT 901
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 QY 902 CTTTCTTTTCTCGATGTACTACATTTGATCTGAGTCAACA 942
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RESULT 6
 AY409412
 LOCUS
 DEFINITION
 Mus musculus COLEC10 gene, VIRUAL TRANSCRIPT, partial sequence.
 genomic survey sequence.
 AY409412
 VERSION
 AY409412.1 GI:39765380
 KEYWORDS
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 ORGANISM
 Mus musculus
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 834)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

QY	666	ATGTTTCACAGACACACTCCACTGCAGAACTATAGCACTCGAATGAGGGACCCAGC	725		
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QY	726	GACCCCTATGCTCATGAGGAACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	785		
Db	721	GACCCCTCGGGCCATGAGGAACTGTGTGGAGATGTTGAGCTCTGGCAGTGAATGACACA	780		
QY	786	GAGTGCCATCTTACCATTGACTTGTCTGTGAGTTTCATCAGAGAGAAAAAGTAA	839		
Db	781	GAGTGTCACCTTACCATTGATTTTGTCTGTGAGTTTGTCAAGAGAGAAAAATAA	834		
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LOCUS	BM010788				
DEFINITION	603629302F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5434680 5', mRNA linear EST 30-OCT-2001				
ACCESSION	BM010788	mRNA sequence.			
VERSION	BM010788.1	GI:16525142			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 609)				
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI912 row: c column: 01 High quality sequence stop: 608.				
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	/clone_lib="NIH MGC 41"				
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	Query Match 35.5%; Score 566.8; DB 12; Length 609;				
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	Matches 590; Conservative 0; Mismatches 2; Indels 2; Gaps 2;				
QY	367	GTGGAAGATACCGGAATTTGTTGGACAACTCGATATTAGTATTGCCCGGCTCAAGACAT	426		
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QY	427	CTATGAAGTTGTCAAGATGTGATAGCAGGAATTAGGGAACCTGAGAGAAATTTACT	486		
Db	61	CTATGAAG-TTGTCAAGATGTGATAGCAGGAATTAGGGAACCTGAGAGAAATTTACT	119		
QY	487	ACATCGTCGAGGAGAGAAACTACAGGGAATTCCTAACCCACTGCAGGATTCGGGGT	546		

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180 GAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCCA 239
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787 AGTGCCATCTTACCATGCTACTTGTCTGTGAGTTCAATCAAGAAAGAAAGTAACTTCCT 846
420 AGTGCCATCTTACCATGCTACTTGTCTGTGAGTTCAATCAAGAAAGAAAGTAACTTCCT 479
847 CATCTACGATTTGCTATTTTCTGTGACCGTCAATCAGATTATGTTATCCATCCTTT 906
480 CATCTACGATTTGCTATTTTCTGTGACCGTCAATCAGATTATGTTATCCATCCTTT 539
907 TTTTCTCTGATGACTACATTTGATCTGAGTCAACATAGCTAGAAATGCTAAA 960
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RESULT 8
BX228545
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CB228545 747 bp mRNA linear EST 10-FEB-2003
AGENCOUT 11505973 NICHDRh_Ovi Macaca mulatta cDNA clone
IMAGE:6886251 5', mRNA sequence.
CB228545
CB228545.1 GI:28280123
EST.
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
1 (bases 1 to 747)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Elliot Spindel
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNC9139 row: a column: 02
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Location/Qualifiers
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pre-pubertal, post pubertal sn menopausal monkeys.

FEATURES
source

ORIGIN

Query Match 31.0%; Score 494.2; DB 14; Length 747;
Best Local Similarity 97.3%; Pred. No. 2,6e-123;
Matches 533; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
441 AGAATGTCATAGCGGATTTAGGGAATCTGAAGAGAAATTTCTACTACATCGTCAGGAA 500
Db 3 AAGAATGTCATAGCGGATTTAGGGAATCTGAAGAGAAATTTCTACTACATCGTCAGGAA 62
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621 CGGGTTCATTTGGCGTGAATGACCTTCAAGAGGAGGACAGTACATGTTCCACAGCAAC 680
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681 ACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGGTCAT 740
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Db 303 GAGGACTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACAGAGTGCATCTTACC 362
801 ATGACTTTGCTGTGAGTTCAATCAAGAAAGAAAGTAACTTCCTCATCTAGCTATTT 860
Db 363 ATGACTTTGCTGTGAGTTCAATCAAGAAAGAAAGTAACTTCCTCATCTAGCTATTT 422
861 GCTATTTTCTGTGACCGTCAATCAGTATTTATCCATCC-TTTTTTTCTGATGTT 919
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920 ACTACATTTGATCTGAGTCAACATAGCTAGAAATGCTAAACTCAGG 966
Db 483 ACTACATTTGATCTGAGTCAACATAGCTAGAAATGCTAAACTCAGG 529

RESULT 9
BX494095
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BX494095 560 bp mRNA linear EST 04-SEP-2003
DKFZp779A1511 x1 779 (synonym: hnccl) Homo sapiens cDNA clone
DKFZp779A1511 5', mRNA sequence.
BX494095
BX494095.1 GI:32007261
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 560)
Fobo, G., Han, M. and Wiemann, S.
Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project..
No 31 sequence available.
This clone (DKFZp779A1511) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Constructed by Clontech. Note: this is a NICHDR Library."

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FEATURES
source
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ORIGIN

Query Match	29.3%;	Score 467.8;	DB 13;	Length 560;
Best Local Similarity	99.6%;	Prod. No. 3.7e-116;		
Matches 469;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	CAGCAATGAATGGCTTTGGCATCTTTGGTTCGAAAGAAACCAATTTATCTCTCGTGACTAT	60	
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QY	241	TGGGTGATATGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG	300	
Db	330	TGGGTGATATGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG	389	
QY	301	ACAAAGGGGAAAAAGTTTGTTGGAATACCTCGAGAAAAAGCGAAACGAGTACTGTCT	360	
Db	390	ACAAAGGGGAAAAAGTTTGTTGGAATACCTCGAGAAAAAGCGAAACGAGTACTGTCT	449	
QY	361	GTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCCCGGCTCA	420	
Db	450	GTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCCCGGCTCA	509	
QY	421	AGACATCTATGAAGTTTCTCAAGAACTGTATGACAGGGATTAGGGAAACTG	471	
Db	510	AGACATCTATGAAGTTTCTCAAGAACTGTATGACAGGGATTAGGGAAACTG	560	

RESULT 10	BB612129	955 bp	linear	EST 31-AUG-2001
LOCUS	BB612129			
DEFINITION	BB612129 RIKEN full-length cDNA clone 443240O08 5'			
ACCESSION	BB612129			
VERSION	BB612129.1			
KEYWORDS	EST.			

SOURCE: Mus musculus (house mouse)
ORGANISM: Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 955)

AUTHORS
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaizaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ico, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, X., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.

TITLE
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL
Unpublished (2001)

COMMENT
Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>,
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Prepare full-length cDNA libraries for cap-trapper-selected cDNAs to
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Matsuhiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.,
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K.,
Arakawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct.
Funct. Genomics* 2 pre, 172-186 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

FEATURES
SOURCE

```

Location/Qualifiers
1. .955
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4432404O08"
/sex="mixed"
/tissue_type="liver"
/dev_stage="14 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 14 days embryo
liver"
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGAGATCCAGAGACTCTTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATTCCTCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I"

```

ORIGIN

Query Match 28.6%; Score 455.8; DB 10; Length 955;
Best Local Similarity 81.7%; Pred. No. 8.4e-113;
Matches 539; Conservative 0; Mismatches 118; Indels 3; Gaps 17

2 AGCAATGAATGCTTTGGCATCTTGGCTTCGAAGAAACCAATTTATCTCTCGTACTATT 61
5 AGTCATGAATGCTTTAGAGTCCCTGCTTCGAAGCAACCTATCAATGCTGTTCTGCTAGC 64


```
62 TCTTTTGCACAAATTCAGAGTCTGGTCTGGATATTGATAGCCCTCTACCGCTGAAGTCTG 121
65 TCTTTTGCACAAATTCAGAGTCTGGTCTGGATATTGATAGCCCTCTACCGCTGAAGTCTG 124
122 TGGCAGACACACAAATTCAGAGTCTGGTCTGGATATTGATAGCCCTCTACCGCTGAAGTCTG 181
125 TGGCAGACACACAAATTCAGAGTCTGGTCTGGATATTGATAGCCCTCTACCGCTGAAGTCTG 184
182 AGAAGAGGGAAGACATGGCAAGTGGGAGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 241
185 AGAAGAGGGAAGACATGGCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 244
242 GGTGTATATGGAGATCGGGGCAATTTGGCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301
245 GGTGTATATGGAGATCGGGGCAATTTGGCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 304
302 CAAAGGGGAAAAAGTGTCTTGGATATCTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361
305 CAAAGGGGAAAAAGTGTCTTGGATATCTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 364
362 TGAATTTGGAGATACCGGAATTTTGGCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421
365 TGAATTTGGAGATACCGGAATTTTGGCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424
422 GACATCTATGAAGTGTCTCAAGATGTGATAGCAGGATTTGGGAAAGTGGGAGGAGGAGGAGGAGG 481
425 GACATCTATGAAGTGTCTCAAGATGTGATAGCAGGATTTGGGAAAGTGGGAGGAGGAGGAGGAGG 484
482 CTACTACATCTGTCAGGAAGAGAACTACAGGGAATCCCTTAACCCCACTGCAGGATTCG 541
485 CTACTACATCTGTCAGGAAGAGAACTACAGGGAATCCCTTAACCCCACTGCAGGATTCG 544
542 GGTGTGAATCTAGCATCCCGAGGATGAAGTCCCAACACATCATCGCTGACTATGT 601
545 AGAGGAGATCTAGCATCTGAGATGCTGAGATGAAGTGTGACACCCCTATTGCTGACTATGT 604
602 TGGCAAGAGTGGTCTCTTTCCGGTGTTCATTTGGTGTGATGACCTTGAAGAGGAGGAGGAGCA 661
605 CGCC---AGAGTGGTCTCAGAGTGTACATGGGGTCTATACCTTGAGAGGAGGAGGAGGAGCA 661
```

```
RESULT 11
LOCUS BX496500 457 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp779M0527.1 779 (synonym: hnccl) Homo sapiens cDNA clone
ACCESSION DKFZp779M0527.5, mRNA sequence.
VERSION BX496500
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M., and Wiemann, S.
EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr. 1, D-85764 Neuherrnberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
Researched by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseeldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No s1 sequence available.
This clone (DKFZp779M0527) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: Clone@rzpd.de.
Location/Qualifiers
1. .457
/organisms="Homo sapiens"
```

```
ORIGIN
Query Match 27.1%; Score 432.8; DB 13; Length 457;
Best Local Similarity 99.5%; Pred. NO. 1.2e-106;
Matches 434; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAGCAATGAATGGCTTTTGCATCTCTTTCGAAAGAACCAATTTATCTCTCTGCTACTAT 60
DB 22 CAGCAATGAATGGCTTTTGCATCTCTTTCGAAAGAACCAATTTATCTCTCTGCTACTAT 81
QY 61 TTTCTTTTGCAAATTCAGAGTCTGGTCTGGATATTGATAGCCCTCTACCGCTGAAGTCT 120
DB 82 TTTCTTTTGCAAATTCAGAGTCTGGTCTGGATATTGATAGCCCTCTACCGCTGAAGTCT 141
QY 121 GTGCCACACACAAATTTTCCAGGAGCCCAAGGAGATGATGGTGAAAAAGGAGATCCAG 180
DB 142 GTGCCACACACAAATTTTCCAGGAGCCCAAGGAGATGATGGTGAAAAAGGAGATCCAG 201
QY 181 GAGAGAGGGAAGCATGGCAAGTGGGAGCCGATGGGCCCGGAAAGGAATTAAGAGGAAC 240
DB 202 GAGAGAGGGAAGCATGGCAAGTGGGAGCCGATGGGCCCGGAAAGGAATTAAGAGGAAC 261
QY 241 TGGGTGATATGGAGATCGGGCAATATTGGCAAGTGGGCCCATTTGGGAGGAAGGGTG 300
DB 262 TGGGTGATATGGAGATCAGGCAATATTGGCAAGTGGGCCCATTTGGGAGGAAGGGTG 321
QY 301 ACAAGGGGAAAAAGTGTCTTGGATATCTTGGAGAAAAAGGCAAGGAGGATCTGTCT 360
DB 322 ACAAGGGGAAAAAGTGTCTTGGATATCTTGGAGAAAAAGGCAAGGAGGATCTGTCT 381
QY 361 GTGATTGTGGAGATACCGGAAATTTTGGCAAGTGGATATTAGTATTCGCCGCTCA 420
DB 382 GTGATTGTGGAGATACCGGAAATTTTGGCAAGTGGATATTAGTATTCGCCGCTCA 441
QY 421 AGACATCTATGAAGTT 436
DB 442 AGACATCTATGAAGTT 457
```

```
RESULT 12
LOCUS BF078010 492 bp mRNA linear EST 18-OCT-2000
DEFINITION 228226 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF078010
VERSION BF078010.1 GI:10871840
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 492)
Fahrenkrug, S.C., Smith, T.P.L., Fekking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,
Quackenbush, J., and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE 22213789
PUBMED 12226715
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
```


Single pass sequencing. Bases called and alt. trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCAGGTCAGGAG

Plate: 49 row: F column: 11

Seq primer: ATTAGGTGACATATAG.

Location/Qualifiers

1. 492

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 2P1G"

/note="Vector: PCW SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from testis, ovary,

endometrium, hypothalamus, pituitary, and placenta."

FEATURES

source

Query Match 26.0%; Score 414.2; DB 10; Length 492;
Best Local Similarity 90.2%; Pred. No. 1.5e-101;
Matches 443; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY	1	CAGCAATCAATGGCTTTCATCTTGTTCGAGAAACCAATTTATCTCTCTGCTACTAT	60
DB	2	CAGCAATGGTGGCTCTGGAGCTCGAAGAACCAATTTATCTCTCTGCTACTAT	61
QY	61	TTCTTTTGAATTCAGAGTCGTGGTCTGGATTTATGATACCGTCTTACCGTGAAGTCT	120
DB	62	TTCTTTTGCAGATTCAGAGTCGTGGTCTGGATTCGATCGACATCGACATCGTCTCT	121
QY	121	GTGCCACACACATTTTCCACGAGCCCAAGGAGATGATGGTGAAGAAAGGAGATCCAG	180
DB	122	GTGCCACACACATTTTCCACGAGCCCAAGGAGATGATGGTGAAGAAAGGAGATCCAG	181
QY	181	GAGAGAGAGGAAGCATCGCAAAAGTGGAGCGCATCGGCGGCAAGAAATTAAGAGGAGAC	240
DB	182	GAGAGAGAGGAAGCATCGCAAAAGTGGAGCGCATCGGCGGCAAGAAATTAAGAGGAGAC	241
QY	241	TGGGTGATATGGAGATCGGCGCAATATGCAAGATCGGCGGCAAGAAATTAAGAGGAGAC	300
DB	242	TGGGTGATATGGAGATCGGCGCAATATGCAAGATCGGCGGCAAGAAATTAAGAGGAGAC	301
QY	301	ACAAAGGGGAAAAGTTTGTCTGGAATACCTGGAGAAAAGGCAAGAGGACTGTCT	360
DB	302	ACAAAGGGGAAAAGTTTGTCTGGAATACCTGGAGAAAAGGCAAGAGGACTGTCT	361
QY	361	GTGATTTGGAGATACCGGAATTTGTGGACAACTGGATTTAGTATTTGCCGCTCA	420
DB	362	GTGATTTGGAGATACCGGAATTTGTGGACAACTGGATTTAGTATTTGCCGCTCA	421
QY	421	AGACATCTATGAATTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAAT	480
DB	422	AGACATCTATGAATTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAAT	481
QY	481	TCTACTATATC	491
DB	482	TCTACTATATC	492

RESULT 13

EX671934

LOCUS

DEFINITION

scac00321.c.03 5prim, mRNA sequence.

EX671934

VERSION

EX671934.1 GI:37984037

KEYWORDS

Sus scrofa (pig)

Sus scrofa

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Bases 1 to 636)

Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,

Soares,M., Bonaldo,F. and Hatey,F.

A Pig Normalised Multi-Tissue cDNA Library

Unpublished (2003)

Contact: Tosser-Klopp G

Genetique Animale

Institut National de la Recherche Agronomique

Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan

cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Clone distribution: AGENAE Resource centre. Francois PIUMI,

Genome PIUMI@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du

germe (UREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,

FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73

sequence cleaned of vector, adaptor and repetitions. Contact us

at signenasupport@jouy.inra.fr to obtain the chromatogram of this

sequence.

Plate: 0032 row: C column: 3.

Location/Qualifiers

1. 636

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/tissue_type="mixed"

/clone_lib="Sus Scrofa library (scac)"

/notes="Vector: pT73D-pac vector; tissues: adipose tissue,

brain, kidney, liver, muscle, ovary, testis, heart,

hypothalamus, pancreas, skin, spleen, thymus, placenta,

pituitary gland, seminal vesicle, small intestine,

uterus, adrenals, bulbo urethral gland, cerebral trunk,

epididymis, female gonad, gall-bladder, hippocampus,

large intestine, male gonad, melanocytes, stomach, udder"

FEATURES

source

ORIGIN

Query Match	25.0%;	Score 398.2;	DB 13;	Length 636;
Best Local Similarity	81.9%;	Pred. No. 3.7e-97;		
Matches	484;	Conservative	0;	Mismatches 103; Indels 4; Gaps 2;
QY	463	GGGAACTGAGAGAAATCTTACTACATCGTCGAGAGAGAACTACAGGAAATCC	522	
DB	1	GGGAACTGAGAGAAATCTTACTATCGTCGAGAGAGAACTACAGGAAATCC	60	
QY	523	TAACTCCACTGACGATTCGGGGTGGAAATCTAGCCATGCCAAGGATGAAGTGC	582	
DB	61	TGACCCACTCCGATCCGGGGGGGATGTAGCCATGCCAAGGAGAGGCTGCCA	120	
QY	583	CATCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTCGGGTGTTTCA	642	
DB	121	CGCTCCTCGCTGACTAGCTCTCCAGAGCGGCTTCTTCGAGTGTTCATCG	180	
QY	643	ACCTTGAAGAGGAGGAGCAGTACATGTTTCCAGACAACTCCACTGCAGAA	702	
DB	181	ACCTGGAGAGGAGGAGGAGCAGTACATGTTTCCAGACAACTCCACTGCAG	240	
QY	703	ACTGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	762	
DB	241	ACTGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	300	
QY	763	GCTCTGGCAGATGGAATGACACACAGTGCATCTTACCATGTACTTTGTCTG	822	
DB	301	GCTCTGGCAGATGGAATGACACACAGTGCATCTTACCATGTACTTTGTCTG	360	
QY	823	TCAAG	882	
DB	361	TCAAG	420	
QY	883	TACAGTTATTTTATTCATCTCTTTTCTCTGATTTTCTTACTTACTTACT	942	

```

1b 421 GGCAGTTATTTTAAATCCACTTTT---CTAATTACATAAATTTGTTCTGACTCAAGG 477
1y 943 TAGCTAGAAATGCTAAACTGAGGTATGGAGCTCCATCATCTCTTTTGTGATGAT 1002
1b 478 CAAGTGAACATGCTAGACTGGGCTTGGAACTCCACTGCCATCGGTGCGTCAAGAT 537
1y 1003 TTTC-ATAATTTTACACATGATGATTTATGACCCCAATTAATCGCCAGGTT 1052
1b 538 TTTCAACATTTCCATACATGGTGTGATATTGAGCCATAAGCTCACCAGGCT 588

RESULT 14
LOCUS   F378429
DEFINITION   CF378429 930 bp mRNA linear EST 27-AUG-2003
AGENCOURT 15349559 NICHHD_XGC_SwblN Silurana tropicalis cDNA clone
IMAGE:7005528 5', mRNA sequence.
ACCESSION   CF378429
VERSION     CF378429.1 GI:34315873
KEYWORDS    EST.
SOURCE      Silurana tropicalis (western clawed frog)
ORGANISM    Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 930)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbe@mail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14704 row: j column: 22
High quality sequence stop: 677.
FEATURES             source
1. .930
   /organism="Silurana tropicalis"
   /mol_type="mRNA"
   /db_xref="taxon:8364"
   /clone="IMAGE:7005528"
   /tissue_types="whole body"
   /clone_lib="NICHHD_XGC_SwblN"
   /notes="Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHHD_XGC_Swbl). Library
was constructed by Open Biosystems (Huntsville, AL)."
```

ORIGIN

```

Query Match      24.9%; Score 396.6; DB 14; Length 930;
Best Local Similarity 68.7%; Pred. No. 1.2e-96;
Matches 546; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

2y 49  TCCCTGGTACTATTTCTTTTGGAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTA 108
1b 102 TCCCTGGGGGTATAGCGCTACATGTGGCTCTCTCTTTGGAGGTGGAGAACATTTCTG 161
2y 109 CCGCTGAAGTGTGGCCACACACACAAATTTTCACAGAGCCCAAGAGAGATGATGGTGA 168
1b 162 CTGTGGATACTTGTTCACACTCACACCACTTCTGCCGGGACCCCAAGGGGATGAGAGAG 221
```

```

169 AAGGAGATCCAGGAGAAGAGGGAAAGCATGGCAAGTGGGCGCATGGGGCGGAAGAA 228
222 CTGGAGATACGGGGGTCTTGGGAAAGCTGGGAAAGATGGACCCCAAGGGGCGAAGGCA 281
229 TTAAGAGGAACCTGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCATTG 288
282 ATAAAGAAATAATAGGGGATTTCTGGGACCTCTGGGCTGTAGTTAAATTTGGCCCAATTG 341
289 GGAGAAGGGTGCACAAAGGGGAAAGGTTTCTTGGAAATACCTGGAGAAAAAGCAAG 348
342 GCAGCAAGGGGATAAAGGACATAAAGGCTTCCCGGCTTCCAGGAGCAAAAGGAAAT 401
349 CAGGTACTCTCTGTGATTTGTGGAAGATACCGGAATTTTGGCAACTGGATATTAGTA 408
402 CAGCGAGTTACTGTGATTTGTGAAGGTACCGCAAGTTGTGGGCGAGCTGGACGTTAATG 461
409 TTGCCCGGCTCAAGACATCTATGAAGTTTGTCAAGATTTGTATAGCAGGGATTAGGAAA 468
462 TTGGCGACCTAAAGTCTTCTTAAATTTGTAATAAATTTGATTGCCGGCATCAGGAAA 521
469 CTGAAGAGAAATTTACTACATCGTGCAGGAAGAGAAAGAACTACAGGGAATCCCTAACCC 528
522 CAGATGAGAAGTACTATTATCATTTGTGAGAGAAGAGCGGAATCTACAGGGATGCGTGA 581
529 ACTGCAGGATTCGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCAACACACTCA 588
582 AGTGTGCGATAGAGGGGTACATTGGCAATGCCCAAGGATCAAGCTACCAATTCCTCA 641
589 TCCTGACTATGTTGCCAAGAGTGGCTTTTCGGGGTGTTCATTGGCGTGAATGACCTTG 648
642 TTGCTGATTACATCTCCAAATGGGGCTTTTTCAGAGTATTTATAGGAATAAATGACATTG 701
649 AAAGGAGGAGCAGTACATGTTTACAGACCAACACTCCACTGCAGAACTATAGCAACTGGA 708
702 AGAAAGAGAGAGATTGTTGATGAGATACTCCCACTGCAGACTTACAGCAGCTGGA 761
709 ATGAGGGGAAACCCAGCGACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTG 768
762 AAGCCGGAGAACCCACACGATGGCTCTGGGTAGCAAGACTGGGTGGAAATGCTCAGCACCG 821
769 GCAGATGGAATGACACAGAGTGCATCTTACCATCTACTTGTCTGTGAGTTTCATCAAGA 828
822 GCCATTGGAGACGACGTGGACTGCAGTCTGACCATCTACTTTGTTGTGAGTTTCTGAAA 881
829 AGAAAAGTAACCTTC 843
882 AGACAAAGTAGCTGC 896
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RESULT 15

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BI467460
LOCUS      389071 MARC 2P1G Sus scrofa cDNA 5', mRNA linear EST 22-AUG-2001
DEFINITION
ACCESSION  BI467460
VERSION    BI467460.1 GI:15280338
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 499)
Fahrenkrug S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,
Quackenbush, J., and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
2213789
12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
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TITLE

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JOURNAL
MEDLINE
PUBMED
COMMENT
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Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG
Plate: 142 row: E column: 10
Seq primer: ATTAGGTGACACTATAG.

FEATURES

source

1. .499
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 2P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Query Match 24.5%; Score 391; DB 12; Length 499;
Best Local Similarity 89.4%; Pred. No. 3.1e-95;
Matches 421; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy	1	CAGCAATGAATGGCTTTGGCATCTTCTCGAAGAAACCAATTTATCCTCTCTGTACTAT	60
Db	29	CAGCAATGGTGGCTTTGGAGCTGGACCTCGAAGAAACCAAGTTCATCTCTCTGGGCTCT	88
Qy	61	TTCTTTTGAATTCAGATCTGGTCTGGATATTGATAGCGCTCCTACCGCTGAAGTCT	120
Db	89	TTCTTTTGCAGATTCAGATCTGGTCTGGATCGACAGTCGTCTACCGCTGAAGTCT	148
Qy	121	GTGCCACACACAAATTCACCAAGACCCCAAGGAGATGATGGTCAAAAAGGATCCAG	180
Db	149	GTGCCACACACAAATTCACCAAGACCCCAAGGAGATGATGGTCAAAAAGGATACAG	208
Qy	181	GAGAAGAGGAAGCATGGCAAGTGGGACGATGGGCGGCAAGGAAATTAAGGAGAAC	240
Db	209	GAGAGAGGGAAGCATGGCAAGTGGGACGATGGGCGGCAAGGAAATTAAGGAGAAC	268
Qy	241	TGGTGATATGGGAGATCGGGCAATATTGGCAAGACTGGGCGCCATTTGGGAAGAGGTG	300
Db	269	TGGTGATATAGAGACCGGCAATATTGGCAAGACTGGGCGCCATTTGGGAAGAGGTG	328
Qy	301	ACAAAGGGGAAAAGGTTTGGTGGAAATACCTGGAGAAAAGGCAAGCAGGTACTGTCT	360
Db	329	ACAAAGGAGAAAAGGGTTTGGTGGAAATACCTGGAGAAAAGGCAAGCAGGTACTGTCT	388
Qy	361	GTGATTGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCCGGTCA	420
Db	389	GTGATTGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCCGGTCA	448
Qy	421	AGACATCTATGAAGTTTGTCAAGATGTGATAGCAGGGAATTAGGGAACCTG	471
Db	449	AGACATCGATGAAGTTTGTCAAGATGTGATAGCAGGGAATTAGGGAACCTG	499

Search completed: February 24, 2004, 00:35:27
Job time : 4313 secs

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;       TELEX:      (216) 980162
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; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 1868 base pairs
;     TYPE: Nucleic acid
;     STRANDEDNESS: Single
;     TOPOLOGY: Linear
;
; MOLECULE TYPE: Nucleotide-genomic DNA
;
; HYPOTHETICAL: No. 5691197 relevant
;
; ANTI-SENSE: No. 5691197 relevant
;
US-08-392-367B-1

Query Match      4.1%;      Score 68.6;      DB 1;      Length 1868;
Best Local Similarity 56.4%;      P: 0;      No. 4.9e-11;
Matches 128;      Conservative 0;      Mismatches 99;      Indels 0;      Gaps 0;

QY      128  ACACACAATTTCACCAGGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGGAGAAGA 187
Db      780  ACTTACGGGTGCACCAGGGAAGCAAGGACCACTGGTCTCCAGGACCTCGAGGAGAGAA 839
QY      198  GGGAAAGCATGGCAAGTGGGACGCATGGGGCCGAAAGGAATTAAAGGAGAACTGGGTGA 247
Db      840  GGGCAGCAAAAGGTGCATAGGTTCTCACTGGCCCCAAGGGGGAACATGGCCACCAAGGGGAGA 899
QY      248  TATGGAGAGATCGGGGCAAAATTATGGCAAGACTGGGGCCCATTTGGGAAGAAGAGGTGACAAAGG 307
Db      900  CAAAGGGGACCTTAGGCTTCCAGGAAACAAGGGGACATGGGCATGAAGGGGACACCGG 959
QY      308  GGAAAAAGGTTTGGTTGGAAATACCTTGGAAAAAAGGCAAAAGCAGGTA 354
Db      960  GCCCATGGGGTCCCTTGGAGCTCAGGAGGTAAAGGTGATGCTCGAA 1006

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RESULT 3
US-08-893-467A-1
Sequence 1, Application US/08893467A
Patent No. 6063901
GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Elomaa, Outi
APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Insolated DNA Sequence For a
Patent No. 6063901
TITLE OF INVENTION: No. 6063901el Macrophage Receptor with
TITLE OF INVENTION: a Collagenous Domain and the
TITLE OF INVENTION: Polypeptide Chain Encoded by
TITLE OF INVENTION: such a Sequence
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Fay, Sharpe, Beall, Fagan,
ADDRESSER: Minnich & McKeel
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 720 Kb storable
COMPUTER: IBM PS/2, Model 35 SX
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,467A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TRV 2 009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582

Db 229 GTATGCCAACAAGGACCC-----TGGATTGGCCCTCCGGACCTGGACAGAGA 179
Qy 656 GGCACAGTACATGTTTACACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 715
Db 178 GGGGAGTTTATCTGATGGACGAGAACCCCT---GAATATAGCAACTGGCGCCGG 122
Qy 716 GGAACCCAGGACCCCTATGGTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATG 775
Db 121 GGAGCCCAACAACGGGGGCCAGGCGGAGGACTGCGTGATGATGACAGGGCTCGGGCAGTG 62
Qy 776 GAATGACACAGAGTGC 791
Db 61 GAATGACGCTTCTGC 46

RESULT 12

US-09-535-521-16
; Sequence 16, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-09-535-521-16

Query Match 4.0%; Score 64; DB 4; Length 561;
Best Local Similarity 55.1%; Pred. No. 6.1e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
Qy 476 GAAATTTCTACTACATCGTCGAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 535
Db 213 GAAGTGCTACTACTTCGGCGAGGAGCCCAAGAGTGGATCCAGGCCGGTTTGCCTGCAG 272
Qy 536 GATTGGGGTGAATGCTAGCTATGCCAGGATGAGCTGCCACACTCATCGCTGA 595
Db 273 CAAGCTGCAAGGGGGCTGCGCCAGCATCCACAGCAAGAGGAGGAGGACTTCTTGGCCAG 332
Qy 596 CTATGTTGCCAAGAGTGGCTTCTTGGGTGTTTCATTGGCGTGAATGACTTTGAAAGGGA 655
Db 333 GTATGCCAACAAGAGGACCC-----TGGATTGGCCCTCCGGACCTGGACAGAGA 383
Qy 656 GGCACAGTACATGTTTACACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 715
Db 384 GGGGAGTTTATCTGATGGACGAGAACCCCT---GAATATAGCAACTGGCGCCGG 440
Qy 716 GGAACCCAGGACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATG 775
Db 441 GGAGCCCAACAACGGGGGCCAGGCGGAGGACTGCGTGATGATGACAGGGCTCGGGCAGTG 500
Qy 776 GAATGACACAGAGTGC 791
Db 501 GAATGACGCTTCTGC 516

RESULT 13

US-09-535-521-18/c
; Sequence 18, Application US/09535521

; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-18

Query Match 4.0%; Score 64; DB 4; Length 561;
Best Local Similarity 55.1%; Pred. No. 6.1e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
Qy 476 GAAATTTCTACTACATCGTCGAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 535
Db 349 GAAGTGCTACTACTTCGGCGAGGAGCCCAAGAGTGGATCCAGGCCGGTTTGCCTGCAG 290
Qy 536 GATTGGGGTGAATGCTAGCCATGCCCAAGATGAAGTCCCAACACACTCATCGCTGA 595
Db 289 CAACTGCAAGGGCGGCTGCCAGCATCCACAGCAAGAGGAGGAGGACTTCTTGGCCAG 230
Qy 596 CTATGTTGCCAAGAGTGGCTTCTTGGGTGTTTCATTGGCGTGAATGACTTTGAAAGGGA 655
Db 229 GTATGCCAACAAGAGGACCC-----TGGATTGGCCCTCCGGACCTGGACAGAGA 179
Qy 656 GGCACAGTACATGTTTACACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 715
Db 178 GGGGAGTTTATCTGATGGACGAGAACCCCT---GAATATAGCAACTGGCGCCGG 122
Qy 716 GGAACCCAGGACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATG 775
Db 121 GGAGCCCAACAACGGGGGCCAGGCGGAGGACTGCGTGATGATGACAGGGCTCGGGCAGTG 62
Qy 776 GAATGACACAGAGTGC 791
Db 61 GAATGACGCTTCTGC 46

RESULT 14

US-09-535-521-19
; Sequence 19, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CDS
; LOCATION: (1)..(624)
US-09-535-521-19

Query Match 4.0%; Score 64; DB 4; Length 624;
Best Local Similarity 55.1%; Pred. No. 6.5e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
QY 476 GAAATTCCTACTACATCGTCGAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 535
DB 276 GAAATTCCTACTACTTCGGCGAGGAGCCCAAGAGTGGATCCAGGCCCGGTTTGCCTGCAG 335
QY 536 GATTCGGGGTGAATGCTAGCATGCTCCAGGATGAAGTCCCAACACACTCATCGCTGA 595
DB 336 CAAGCTGCAAGGGCGGCTGGCCAGCATCCACAGCAAGAGGAGGAGCTTCTGGCCAG 395
QY 596 CTATGTTCCCAAGAGTGGCTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 655
DB 396 GTATGCCAACAAAGAGGGCACCC-----TGGATTGGCTCCGGGACCTGGACACAGA 446
QY 656 GGGACAGTACATGTTTCAGACACACACTCCACATGCAGAACTATAGCAACTGGGAATGAGGG 715
DB 447 GGGGAGTTTATCTGGATGGACGAGAACCCCT---GAACTATAGCAACTGGCGGCCCGG 503
QY 716 GGAACCCAGCGACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATG 775
DB 504 GGAGCCCAACAACGGGGCCAGGGCGAGGACTGGGTGATGATGACAGGGCTCGGGGCAGTG 563
QY 776 GAATGACACAGAGTGC 791
DB 564 GAATGACGCTTCTGC 579

RESULT 15
US-09-535-521-21/c
; Sequence 21, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY ICE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-21

Query Match 4.0%; Score 64; DB 4; Length 624;
Best Local Similarity 55.1%; Pred. No. 6.5e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
QY 476 GAAATTCCTACTACATCGTCGAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 535
DB 349 GAAATTCCTACTACTTCGGCGAGGAGCCCAAGAGTGGATCCAGGCCCGGTTTGCCTGCAG 290
QY 536 GATTCGGGGTGAATGCTAGCATGCTCCAGGATGAAGTCCCAACACACTCATCGCTGA 595
DB 289 CAAGCTGCAAGGGCGGCTGGCCAGCATCCACAGCAAGAGGAGGAGCTTCTGGCCAG 230
QY 596 CTATGTTCCCAAGAGTGGCTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 655
DB 229 GTATGCCAACAAAGAGGGCACCC-----TGGATTGGCTCCGGGACCTGGACACAGA 179
QY 656 GGGACAGTACATGTTTCAGACACACACTCCACTCAGAACTATAGCAACTGGGAATGAGGG 715
DB 178 GGGGAGTTTATCTGGATGGACGAGAACCCCT---GAACTATAGCAACTGGCGGCCCGG 122
QY 716 GGAACCCAGCGACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATG 775

Db 121 GGAGCCCAACACACGGGGGCCAGGGCGAGGACTGCGTGATGATGACAGGGCTCGGGGCAGTG 62
QY 776 GAATGACACAGAGTGC 791
DB 61 GAATGACGCTTCTGC 46
Search completed: February 24, 2004, 02:09:38
Job time : 126 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 23:23:31 ; Search time 563 Seconds

(without alignments)
9920.289 Million cell updates/sec

Title: US-09-600-932-1

Perfect score: 1595

Sequence: 1 cagcaatgaatggtttgca.....gatttaagaaaaacggagcc 1595

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	980.2	61.5	1016	9	US-09-978-697-96
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4	980.2	61.5	1016	9	US-09-993-832A-96
5	980.2	61.5	1016	10	US-09-978-189-96
6	980.2	61.5	1016	10	US-09-978-608A-96
7	980.2	61.5	1016	10	US-09-978-585A-96
8	980.2	61.5	1016	10	US-09-978-191A-96
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11	980.2	61.5	1016	10	US-09-999-833A-96
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16	980.2	61.5	1016	10	US-09-978-193A-96
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44	980.2	61.5	1016	14	US-10-180-557-99
45	980.2	61.5	1016	14	US-10-173-700-99

ALIGNMENTS

RESULT 1

US-09-978-295A-96
; Sequence 96, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Steward, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630Fic11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

[illegible]

Query Match 61.5%; Score 980.2; DB 9; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAATGATGGCTTTCATCCCTTCTCGAAGAAACCAATTTATCCTCTCGTACTAT 60
DB 17 CAGCAATGATGGCTTTCATCCCTTCTCGAAGAAACCAATTTATCCTCTCGTACTAT 76
QY 61 TTCCTTTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTACCGCTGAAGTCT 120
DB 77 TTCCTTTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTACCGCTGAAGTCT 136
QY 121 GTGCCACACACAAATTTCCAGAGACCCCAAGAGATGATGGTGAAAAAGGAGATCCAG 180
DB 137 GTGCCACACACAAATTTCCAGAGACCCCAAGAGATGATGGTGAAAAAGGAGATCCAG 196
QY 181 GAGAGAGGAAAGATGCGCAAGTGGGACGCGATGGGCGCCGAAAGGAATTTAAAGGGAAC 240
DB 197 GAGAGAGGAAAGATGCGCAAGTGGGACGCGATGGGCGCCGAAAGGAATTTAAAGGGAAC 256
QY 241 TGGGTGATATGGAGATCGGGCAATATTTGGCAAGATCGGGCCCATTTGGGAAGAGGGTG 300
DB 257 TGGGTGATATGGAGATCAGGGCAATATTTGGCAAGATCGGGCCCATTTGGGAAGAGGGTG 316
QY 301 ACAAGGGGAAAGATTTGCTTGAATACCTGGAGAAAAAGGCAAGGAGGACTCTCTCT 360
DB 317 ACAAGGGGAAAGATTTGCTTGAATACCTGGAGAAAAAGGCAAGGAGGACTCTCTCT 376
QY 361 GTGATTTGCAAGATACCGGAAATTTGTTGGCAACTCGGATATTAGTATTTGCCCGGCTCA 420
DB 377 GTGATTTGCAAGATACCGGAAATTTGTTGGCAACTCGGATATTAGTATTTGCCCGGCTCA 436
QY 421 AGACATCTATGAATTTGTCAGAAATGTCATAGCAGGGAATTAGGGAACCTGAAGAGAAAT 480
DB 437 AGACATCTATGAATTTGTCAGAAATGTCATAGCAGGGAATTAGGGAACCTGAAGAGAAAT 496
QY 481 TCTACTATATCTGTCAGGAAGAGAAAGAACTACAGGGAATCCCTAACCCACTGCGAGGATTC 540
DB 497 TCTACTATATCTGTCAGGAAGAGAAAGAACTACAGGGAATCCCTAACCCACTGCGAGGATTC 556
QY 541 GGGGTGGAATGTCAGGATCCCAAGGATGAAGTGCACCAACACACTATCGCTCACTATG 600
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QY 601 TTGCCAAGAGTGGCTTCTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAAGGGAGGGAC 660
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QY 661 AGTACATGTTTCAGACACACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGGAAC 720
DB 677 AGTACATGTTTCAGACACACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGGAAC 736
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QY 781 ACACAGAGTGCATCTTACCATGCTACTTTGCTCTGTGAGTTTCATCAGAGAGAAAAAGTAC 840
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RESULT 2
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; Sequence 96, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrata, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630FIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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141 PRIOR FILING DATE: 1998-05-15
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144 PRIOR APPLICATION NUMBER: 60/085573
145 PRIOR FILING DATE: 1998-05-15
146 PRIOR APPLICATION NUMBER: 60/085704

Query Match 61.5%; Score 980.2; DB 9; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

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DB	77	TTCTTTTCAAAATTCAGAGTCTGGTCTGGATATTGATAGCCGTCCTACCGCTGAAGTCT	136
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QY	181	GAGAAAGGGAAGCATGGCAAAAGTGGACGCAATGGGGCCGAAAGGAATTAAGGGAAC	240
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QY	301	ACAAAGGGGAAAGAGTTTGTCTGGAAATACCTGGAGAAAGGCAAGCAGGTACTGTCT	360
DB	317	ACAAAGGGGAAAGAGTTTGTCTGGAAATACCTGGAGAAAGGCAAGCAGGTACTGTCT	376
QY	361	GTGATTGTGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATTGCCCCGCTCA	420
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DB	557	GGGGTGAATGTACCATGCCATGCCAAGAGTGAAGTGCACACACTCATCGTGAATG	616
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DB	617	TTGCCAAGAGTGGCTTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGAGGAC	676
QY	661	AGTACATGTCACAGACACACTCCACTGCAGACTATAGCAACTGGAATGAGGGGGAAC	720
DB	677	AGTACATGTCACAGACACACTCCACTGCAGACTATAGCAACTGGAATGAGGGGGAAC	736
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DB	737	CCAGCGACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCGGCAGATGAATG	796
QY	781	ACACAGATGCCAATTACCAATGACTTTGTCTGTGAGTTTCATCAAGAGAAAGTAAC	840
DB	797	ACACAGATGCCAATTACCAATGACTTTGTCTGTGAGTTTCATCAAGAGAAAGTAAC	856
QY	841	TTCCCTCATCTTACCTATTTGCTATTTTCCTGTGACCGCTCATACAGTTATTGTTATCA	900
DB	857	TTCCCTCATCTTACCTATTTGCTATTTTCCTGTGACCGCTCATACAGTTATTGTTATCA	916
QY	901	TCCTTTTTTCTGATGCTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA	960
DB	917	TCCTTTTTTCTGATGCTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA	976
QY	961	CTGAGGTATGGAGCCCTCCATCATCA	985

Db 977 CTGAGGTATGGAGCCCTCCATCATCA 1001

RESULT 3
US-09-978-192A-96
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630F1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Query Match 61.5%; Score 980.2; DB 9; Length 1016;

Best Local Similarity 99.7%; Pred. No. 4.5e-290; Mismatches 3; Indels 0; Gaps 0;

Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAATGAATGGCTTTGTCATCCTTCGAGAGAAACCAATTTATCCTCTGGTACTAT 60

Db 17 CAGCAATGAATGGCTTTGTCATCCTTCGAGAGAAACCAATTTATCCTCTGGTACTAT 76

Qy 61 TTCTTTTGCATTCAGAGTCTGGGCTTCGATATTCATAGCCGCTCTACCCGCTGAAGTCT 120

Db 77 TTCTTTTGCATTCAGAGTCTGGGCTTCGATATTCATAGCCGCTCTACCCGCTGAAGTCT 136

Qy 121 GTGCCACACACACAATTTTACCAGGAGGAGATGATGCTGTAAGAGAGATCCAG 180

Db 137 GTGCCACACACATTTCCAGGACCCCAAGAGATGATGTTCAAAAAGAGATCCAG 196
Qy 181 GAGAGAGGAAAGCATGGCAAAAGTGGGACCCATGGGGCCGAAAGGAATTAAGGAGAAC 240
Db 197 GAGAGAGGAAAGCATGGCAAAAGTGGGACCCATGGGGCCGAAAGGAATTAAGGAGAAC 256
Qy 241 TGGGTGATATGGAGATCGGGGCAATATTTGCAAGATCGGCCCATTTGGCAAGAGGGTG 300
Db 257 TGGGTGATATGGAGATCAGGGCAATATTTGCAAGATCGGCCCATTTGGCAAGAGGGTG 316
Qy 301 ACAAGGGGAAAGGTTTGTCTGGAATCTCTGAGAAAGGCAAGCAGGACTGTCT 360
Db 317 ACAAGGGGAAAGGTTTGTCTGGAATCTCTGAGAAAGGCAAGCAGGACTGTCT 376
Qy 361 GTGATTGGAGATACCGGAAATTTGTTGACAACTGGATATTAGTATTGCGCGCTCA 420
Db 377 GTGATTGGAGATACCGGAAATTTGTTGACAACTGGATATTAGTATTGCGCGCTCA 436
Qy 421 AGACATCTATGAAGTTTCTCAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT 480
Db 437 AGACATCTATGAAGTTTCTCAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAAT 496
Qy 481 TCTACTACATCGTCAGAGAGAGAGACTACAGGATCCCTAACCCACTGAGGATTC 540
Db 497 TCTACTACATCGTCAGAGAGAGAGACTACAGGATCCCTAACCCACTGAGGATTC 556
Qy 541 GGGGTGGAATGTACCCATGCCAAGATGAAGCTGCCAACACACTCATCGCTGACTATG 600
Db 557 GGGGTGGAATGTACCCATGCCAAGATGAAGCTGCCAACACACTCATCGCTGACTATG 616
Qy 601 TTGCCAAGAGTGCTCTTGGGTGTTTCATGGCGTGAATGACCTTGAAGAGGAGGAC 660
Db 617 TTGCCAAGAGTGCTCTTGGGTGTTTCATGGCGTGAATGACCTTGAAGAGGAGGAC 676
Qy 661 AGTACATGTTACAGACAACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAC 720
Db 677 AGTACATGTTACAGACAACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAC 736
Qy 721 CCAGGACCCCTATGGTCATGAGGACTGTGTGAGATGCTGAGCTTGGCAGATGGAATG 780
Db 737 CCAGGACCCCTATGGTCATGAGGACTGTGTGAGATGCTGAGCTTGGCAGATGGAATG 796
Qy 781 ACACAGATGCCATCTTACCATGTTGCTGCTGAGTTCATCAAGAGAAAGTAA 840
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Qy 841 TTCCCTCATCTTACGTAATTTGCTATTTTCTGTGACCGTCATTCACGTTATTTGTTATCCA 900
Db 857 TTCCCTCATCTTACGTAATTTGCTATTTTCTGTGACCGTCATTCACGTTATTTGTTATCCA 916
Qy 901 TCCCTTTTCTGATCTTACTACATTTGATCTGAGTCACATAGCTGAATGCTTAA 960
Db 917 TCCCTTTTCTGATCTTACTACATTTGATCTGAGTCACATAGCTGAATGCTTAA 976
Qy 961 CTGAGTATGGAGCCCTCCATCATCA 985
Db 977 CTGAGTATGGAGCCCTCCATCATCA 1001

RESULT 4

US-09-999-832A-96
; Sequence 96, Application US/09999832A
; Publication No. US20020192706A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 61.5%; Score 980.2; DB 9; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAATGAATGGCTTTGGCATCTTGGTTCGAGAAACCAATTTATCTCTCTGGTACTAT 60
Db 17 CAGCAATGAATGGCTTTGGCATCTTGGTTCGAGAAACCAATTTATCTCTCTGGTACTAT 76
Qy 61 TTCTTTTGCATTTAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGCTGAAGTCT 120
Db 77 TTCTTTTGCATTTAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGCTGAAGTCT 136
Qy 121 GTGCCACACACAAATTTACAGGACCCAAAGGAGATGATGGTGAAGAGGAGATCCAG 180
Db 137 GTGCCACACACAAATTTACAGGACCCAAAGGAGATGATGGTGAAGAGGAGATCCAG 196
Qy 181 GAGAAAGAGGAAAGACATGGCAAGTGGGACCGATGGGGCCGAAAGCAATTTAAAGGAGAAC 240
Db 197 GAGAAAGAGGAAAGACATGGCAAGTGGGACCGATGGGGCCGAAAGCAATTTAAAGGAGAAC 256
Qy 241 TGGGTGATATGGGAGATCGGGGCAATTTGGCAGACTGGGCCCATTTGGGAGAGAGGGTG 300
Db 257 TGGGTGATATGGGAGATCAGGGCAATTTGGCAGACTGGGCCCATTTGGGAGAGAGGGTG 316
Qy 301 ACAAGGGGAAAAAGTTTTCCTTGGATACCTCGAGAAAAAGCAAGCAAGTACTGTCT 360
Db 317 ACAAGGGGAAAAAGTTTTCCTTGGATACCTCGAGAAAAAGCAAGTACTGTCT 376
Qy 361 GTGATTGTGGAAGATACCGGAATTTTGTGGCAACTGGATATTAGTATTGCCCCGCTCA 420

Db 377 GTGATGTGGAGATACCGGAATTTGTGGACAACCTGGATATTAGTATTGCTCGGCTCA 436
QY 421 AGACATCTATGAAGTTTGTCAAGAAATGTATGACAGGATTTAGGGAACCTGAAGAGAAAT 480
Db 437 AGACATCTATGAAGTTTGTCAAGAAATGTATGACAGGATTTAGGGAACCTGAAGAGAAAT 496
QY 481 TCTACTACATCGTGAGGAAGAGAACTACAGGGAATCCCTAACCCACTCGAGGATTC 540
Db 497 TCTACTACATCGTGAGGAAGAGAACTACAGGGAATCCCTAACCCACTCGAGGATTC 556
QY 541 GGGGTGGAATGTACCATGCCCAAGAGTGAAGCTGCCAACACACTCATCGCTGACTATG 600
Db 557 GGGGTGGAATGTACCATGCCCAAGAGTGAAGCTGCCAACACACTCATCGCTGACTATG 616
QY 601 TTGCCAAGAGTGGCTCTCTTGGGTTCATTTGGCGTGAATGACCTTGAAGAGGAGGAC 660
Db 617 TTGCCAAGAGTGGCTCTCTTGGGTTCATTTGGCGTGAATGACCTTGAAGAGGAGGAC 676
QY 661 AGTACATGTTCACACACAACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAC 720
Db 677 AGTACATGTTCACACACAACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAC 736
QY 721 CACGACACCCCTATCGTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 780
Db 737 CCAGCGACCCCTATCGTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 796
QY 781 ACACAGAGTGCATCTTACCATGTACTTTGTCTGTGATTCATCAACAGAAAGATTAAC 840
Db 797 ACACAGAGTGCATCTTACCATGTACTTTGTCTGTGATTCATCAACAGAAAGATTAAC 856
QY 841 TTCCCTACCTACGATTTTGTCTATTTTCCCTGTGACCGTCAATACAGTTATTTGTTATCCA 900
Db 857 TTCCCTACCTACGATTTTGTCTATTTTCCCTGTGACCGTCAATACAGTTATTTGTTATCCA 916
QY 901 TCTTTTTTCTGATTTGTACTACATTTTGTCTGATTCATCAACAGTACAGTAAATGCTAAA 960
Db 917 TCTTTTTTCTGATTTGTACTACATTTTGTCTGATTCATCAACAGTACAGTAAATGCTAAA 976
QY 961 CTGAGTATGAGGCTCCCATCATCA 985
Db 977 CTGAGTATGAGGCTCCCATCATCA 1001

RESULT 5

US-09-978-189-96

Sequence 96, Application US/09978189

Publication No. US20030004102A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077450
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;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.5%; Score 980.2; DB 10; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	CAGCAATGAATGGCTTTGTCATCTCTTCTCGAAGAACCAATTTATCTCTCTGGTACTAT	60
DB	17	CAGCAATGAATGGCTTTGTCATCTCTTCTCGAAGAACCAATTTATCTCTCTGGTACTAT	76
QY	61	TTCTTTTGCATAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTACCGTGAAGTCT	120
DB	77	TTCTTTTGCATAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTACCGTGAAGTCT	136
QY	121	GTGCCACACACACAAATTCACAGGACCCCAAGGACATGATGTGAAAAGGAGATCCAG	180
DB	137	GTGCCACACACACAAATTCACAGGACCCCAAGGACATGATGTGAAAAGGAGATCCAG	196
QY	181	GAGAAGAGGGGAAAGCATGGCAAAAGTGGGACGCAATGGGGCCGAAAGAAATTAAGAGAAAC	240
DB	197	GAGAAGAGGGGAAAGCATGGCAAAAGTGGGACGCAATGGGGCCGAAAGAAATTAAGAGAAAC	256
QY	241	TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTTG	300
DB	257	TGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGGCCCATTTGGGAAGAGGTTG	316
QY	301	ACAAAGGGGAAAGGTTTCTTGGATACCTCGAGAAAAGGCAAGCAGGTACTGTCT	360
DB	317	ACAAAGGGGAAAGGTTTCTTGGATACCTCGAGAAAAGGCAAGCAGGTACTGTCT	376
QY	361	GTGATTTGGAAGATACCGGAATTTTGTGGACACTGGATATTAGTATGCCCCGTCA	420
DB	377	GTGATTTGGAAGATACCGGAATTTTGTGGACACTGGATATTAGTATGCCCCGTCA	436
QY	421	AGACATCTATGAGTTTGTCAAGAAATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAAT	480
DB	437	AGACATCTATGAGTTTGTCAAGAAATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAAT	496
QY	481	TCTACTACATCGTCAGGAAGAGAAACTATACAGGGAATCCCTAACCCACTCAGGATTC	540
DB	497	TCTACTACATCGTCAGGAAGAGAAACTATACAGGGAATCCCTAACCCACTCAGGATTC	556
QY	541	GGGGTGGAAATGCTAGCCATCCCAAGGATGAAGTCAAGTGCACACACTCATCGCTGACTATG	600
DB	557	GGGGTGGAAATGCTAGCCATCCCAAGGATGAAGTGCACACACTCATCGCTGACTATG	616
QY	601	TTGCCAAGAGTGGCTTCTTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGGAGAC	660

Db 617 TTGCCAAGTGGCTTTCTTGGGTTTCATTTGGCGTGAATGACCTTGAAGAGGAGGAC 676
QY 661 AGTACATGTTCCACAGCAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 720
Db 677 AGTACATGTTCCACAGCAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAC 736
QY 721 CCAGGAGCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 780
Db 737 CCAGGAGCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 796
QY 781 ACACAGATGGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAGTAAC 840
Db 797 ACACAGATGGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAGTAAC 856
QY 841 TTCCCTCATCTTACATGTTTCTATTTTCCCTGTGACCGTCACTTACAGTTATTGTTATCCA 900
Db 857 TTCCCTCATCTTACATGTTTCTATTTTCCCTGTGACCGTCACTTACAGTTATTGTTATCCA 916
QY 901 TCCTTTTTTTCCTGATTTGATCTTACATTTGATCTGAGTCAACATAGCTAGAAATGCTTAA 960
Db 917 TCCTTTTTTTCCTGATTTGATCTTACATTTGATCTGAGTCAACATAGCTAGAAATGCTTAA 976
QY 961 CTGAGGTATGGAGCCTCCATCATCA 985
Db 977 CTGAGGTATGGAGCCTCCATCATCA 1001

RESULT 6

US-09-978-608A-96
; Sequence 96, Application US/09978608A
; GENERAL INFORMATION:
; Publication No. US20030045462A1
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-96

Query Match 61.5%; Score 980.2; DB 10; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAATCAATGGCTTTTGGCATCTTGTCTCGAAGAAACCAATTTATCTCTCGTACTAT 60
Db 17 CAGCAATCAATGGCTTTTGGCATCTTGTCTCGAAGAAACCAATTTATCTCTCGTACTAT 76
QY 61 TTCTTTTGCATAATTCAGAGTCTGGGTCTGGATATTTGATAGCCCTCTACCGTGAAGTCT 120
Db 77 TTCTTTTGCATAATTCAGAGTCTGGGTCTGGATATTTGATAGCCCTCTACCGTGAAGTCT 136
QY 121 GTGCCACACACACAATTTCCACAGGACCCCAAGAGATGATGCTGAAAAGAGAGATCCAG 180
Db 137 GTGCCACACACACAATTTCCACAGGACCCCAAGAGATGATGCTGAAAAGAGAGATCCAG 196
QY 181 GAGAGAGGGGAAACATGCGCAAGTGGGACGCTATGGGGCCGAAAGGAAATTAAGAGAGAAC 240
Db 197 GAGAGAGGGGAAACATGCGCAAGTGGGACGCTATGGGGCCGAAAGGAAATTAAGAGAGAAC 256
QY 241 TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGGCCCATTTGGGAAGAGGGTG 300
Db 257 TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGGCCCATTTGGGAAGAGGGTG 316
QY 301 ACAAAGGGGAAAAAGTTTCTTGGAAATACCTGGAGAAAAAGCAAGCAGGTACTGTCT 360
Db 317 ACAAAGGGGAAAAAGTTTCTTGGAAATACCTGGAGAAAAAGCAAGCAGGTACTGTCT 376
QY 361 GTGATTGTGGAAGATACCGGAAATTTCTTGGACAACCTGGATATTAGTATTCGCCGCTCA 420
Db 377 GTGATTGTGGAAGATACCGGAAATTTCTTGGACAACCTGGATATTAGTATTCGCCGCTCA 436
QY 421 AGACATCTATGAAGTTTGTCAAGAATGTATAGCAGGGATTAGCGAAACTGAAGAGAAAT 480
Db 437 AGACATCTATGAAGTTTGTCAAGAATGTATAGCAGGGATTAGCGAAACTGAAGAGAAAT 496
QY 481 TCTACTACATCGTCGAGGAGAGAACTACAGGGAATCCCTAAACCCCTGACGATTC 540
Db 497 TCTACTACATCGTCGAGGAGAGAACTACAGGGAATCCCTAAACCCCTGACGATTC 556
QY 541 GGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGTGAATG 600
Db 557 GGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGTGAATG 616
QY 601 TTGCCAAGAGTGGCTTTCTTTGGGTGTTTCAATTTGGCGTGAATGACCTTGAAGCGAGGAC 660
Db 617 TTGCCAAGAGTGGCTTTCTTTGGGTGTTTCAATTTGGCGTGAATGACCTTGAAGCGAGGAC 676
QY 661 AGTACATGTTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAAC 720
Db 677 AGTACATGTTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAAC 736
QY 721 CCAGGAGCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 780
Db 737 CCAGGAGCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 796
QY 781 ACACAGAGTGCCATCTTACCATGTACTTTCTGTGTGAGTTTCATCAAGAGAAAGTAAC 840
Db 797 ACACAGAGTGCCATCTTACCATGTACTTTCTGTGTGAGTTTCATCAAGAGAAAGTAAC 856
QY 841 TTCCCTCATCTAGTATTTGCTATTTTCTGTGACCGTCACTTACAGTTATTGTTATCCA 900
Db 857 TTCCCTCATCTAGTATTTGCTATTTTCTGTGACCGTCACTTACAGTTATTGTTATCCA 916
QY 901 TCCTTTTTTTCCTGATTTGATCTGATTTGATCTGAGTCAACATAGCTAGAAATGCTTAA 960
Db 917 TCCTTTTTTTCCTGATTTGATCTGATTTGATCTGAGTCAACATAGCTAGAAATGCTTAA 976
QY 961 CTGAGGTATGGAGCCTCCATCATCA 985
Db 977 CTGAGGTATGGAGCCTCCATCATCA 1001

RESULT 7
US-09-978-585A-96
; Sequence 96, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978.585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-96

Query Match 61.5%; Score 980.2; DB 10; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	CAGCAATGAATGGCTTTCATCTGCTTTCGAGAAACCAATTTATCTCTCTGCTACTAT	60
DB	17	CAGCAATGAATGGCTTTCATCTGCTTTCGAGAAACCAATTTATCTCTCTGCTACTAT	76
QY	61	TTCTTTTGCATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTACCGTGAAGTCT	120
DB	77	TTCTTTTGCATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTACCGTGAAGTCT	136
QY	121	GTGCGACACACACATTTCCAGAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAG	180
DB	137	GTGCGACACACACATTTCCAGAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAG	196
QY	181	GAGAGAGAGAGAGATGCGCAAGTGGGACGCGATGGGGCCGCAAGGAATTAAGAGGAG	240
DB	197	GAGAGAGAGAGAGATGCGCAAGTGGGACGCGATGGGGCCGCAAGGAATTAAGAGGAG	256
QY	241	TGGGTGATATGGGATCGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTG	300
DB	257	TGGGTGATATGGGATCGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTG	316
QY	301	ACAAAGGGGAAAAAGGTTTGCTTTGGAATACCTGGAGAAAAAGGCAAGACGAGTACTGTCT	360
DB	317	ACAAAGGGGAAAAAGGTTTGCTTTGGAATACCTGGAGAAAAAGGCAAGACGAGTACTGTCT	376

QY	361	GTGATTGTGGAAGATACCGGAATTTGTGTGCAACTGGATATTAGTATTCGCCGGCTCA	420
DB	377	GTGATTGTGGAAGATACCGGAATTTGTGTGCAACTGGATATTAGTATTCGCCGGCTCA	436
QY	421	AGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGATTAAGGAAACTGAAGAGAAAT	480
DB	437	AGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGATTAAGGAAACTGAAGAGAAAT	496
QY	481	TCTACTACATCGTGAGGAGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGATTTC	540
DB	497	TCTACTACATCGTGAGGAGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGATTTC	556
QY	541	GGGTGTGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATG	600
DB	557	GGGTGTGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATG	616
QY	601	TTGCCAAGAGTGGCTTCTTTTCGGGTGTTCATTTGGCGTGAATGACCTTGAAGGGAGGAC	660
DB	617	TTGCCAAGAGTGGCTTCTTTTCGGGTGTTCATTTGGCGTGAATGACCTTGAAGGGAGGAC	676
QY	661	AGTACATGTTTCACAGACAAACACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAC	720
DB	677	AGTACATGTTTCACAGACAAACACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAC	736
QY	721	CCAGCGACCCCTATGCTATGAGGACTGTGTGAGATGCTGAGCTCTGCAGATGGAATG	780
DB	737	CCAGCGACCCCTATGCTATGAGGACTGTGTGAGATGCTGAGCTCTGCAGATGGAATG	796
QY	781	ACACAGAGTGGCATCTTACCATGTACTTTCTGTGTGAGTTTCATCAAGAGAAAAAGTAAC	840
DB	797	ACACAGAGTGGCATCTTACCATGTACTTTCTGTGTGAGTTTCATCAAGAGAAAAAGTAAC	856
QY	841	TTCCCTCATCTACGATTTTGTCTATTTTCTGTGACCGTCATCAGTTATTGTTATCCA	900
DB	857	TTCCCTCATCTACGATTTTGTCTATTTTCTGTGACCGTCATCAGTTATTGTTATCCA	916
QY	901	TCCTTTTTTCTGATTTGACTACATTTGATCTGAGTCAACATAGCTAGAAAATCTAAA	960
DB	917	TCCTTTTTTCTGATTTGACTACATTTGATCTGAGTCAACATAGCTAGAAAATCTAAA	976
QY	961	CTGAGGTATGAGCGCTCCATCATCA 985	
DB	977	CTGAGGTATGAGCGCTCCATCATCA 1001	

RESULT 8
US-09-978-191A-96
; Sequence 96, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
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PRIOR APPLICATION NUMBER: 60/079689
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PRIOR FILING DATE: 1998-03-27
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QY	661	AGTACATGTTACACAGACAAACATCCATCGAGAACTATAGCAACTCGAATGAGGGGAAC	720
DB	677	AGTACATGTTACACAGACAAACATCCATCGAGAACTATAGCAACTCGAATGAGGGGAAC	736
QY	721	CCAGGACCCCTATGGTTCATGAGACCTGTGTGAGATGCTGAGCTCTGGCAGATGGAATG	780
DB	737	CCAGGACCCCTATGGTTCATGAGACCTGTGTGAGATGCTGAGCTCTGGCAGATGGAATG	796
QY	781	ACACAGAGTGGCATCTTTACCAATGTAATTTCTGTGTGAGTTCATCAAGAGAAAAAATAC	840
DB	797	ACACAGAGTGGCATCTTTACCAATGTAATTTCTGTGTGAGTTCATCAAGAGAAAAAATAC	856
QY	841	TTCCCTCATCTACGTATTTTGTCTATTTTCTGTGACCGTCAATACAGTATTGTTATCCA	900
DB	857	TTCCCTCATCTACGTATTTTGTCTATTTTCTGTGACCGTCAATACAGTATTGTTATCCA	916
QY	901	TCCTTTTTTCTGATGTGACTACATTTGATCTGTGATCAACATAGTACAGAAATGCTAAA	960
DB	917	TCCTTTTTTCTGATGTGACTACATTTGATCTGTGATCAACATAGTACAGAAATGCTAAA	976
QY	961	CTGAGTATGAGCTCCCATCATCA 985	
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; Sequence 96, Application US/09978403A			
; Publication No. US20030050240A1			
; GENERAL INFORMATION:			
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; APPLICANT: Baker Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan			
; APPLICANT: Ferrara, Napoleon			
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; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Shelton, David L.			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: P2630PIC17			
; CURRENT APPLICATION NUMBER: US/09/978,403A			
; CURRENT FILING DATE: 2002-03-19			
; PRIOR APPLICATION NUMBER: 09/918585			
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Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 77 TTCTTTTGCATTCAGAGTCTGGGTCTGGATATGATAGCGTCTTACCGCTGAAGTCT 136

QY 121 GTGCCACACACAAATTCACAGGACCCAAAGGAGATGATGTTGAAAAGAGATCCAG 180
DB 137 GTGCCACACACAAATTCACAGGACCCAAAGGAGATGATGTTGAAAAGAGATCCAG 196

QY 181 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
DB 197 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 256

QY 241 TGGGTGATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 300
DB 257 TGGGTGATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 316

QY 301 ACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 317 ACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 376

QY 361 GTGATTTGGAAGATACCGGAATTTTGGCAACTGATATTTAGTATGTCGCCGGCTCA 420
DB 377 GTGATTTGGAAGATACCGGAATTTTGGCAACTGATATTTAGTATGTCGCCGGCTCA 436

QY 421 AGACATCTATGAATTTGTCAAGATGTGTACAGGATTTAGGAACTGAAGAGAAAT 480
DB 437 AGACATCTATGAATTTGTCAAGATGTGTACAGGATTTAGGAACTGAAGAGAAAT 496

QY 481 TCTACTATCTGCAGAGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC 540
DB 497 TCTACTATCTGCAGAGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC 556

QY 541 GGGGTGAATCTAGCATGCCCAAGGATGAAGTGCACACACTATCGCTGACTATG 600
DB 557 GGGGTGAATCTAGCATGCCCAAGGATGAAGTGCACACACTATCGCTGACTATG 616

QY 601 TTGCCAAGTGGCTTTCTTGGGTGTTTCTGCGTGAATGACCTTGAAGGAGGAGGAC 660
DB 617 TTGCCAAGTGGCTTTCTTGGGTGTTTCTGCGTGAATGACCTTGAAGGAGGAGGAC 676

QY 661 AGTACATGTTCCACAGACAACTCCATCTGCAGAACTATAGCAACTGGAATGAGGGGAAAC 720
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QY 721 CCAGGACCCCTATGTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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QY 781 ACACAGAGTGCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAGAAAGTAAC 840
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QY 841 TTCCCTCATCTACGATTTTCTGTTGACCGTCAATTACAGTTATTGTTATCCA 900
DB 857 TTCCCTCATCTACGATTTTCTGTTGACCGTCAATTACAGTTATTGTTATCCA 916

QY 901 TCCTTTTCTGATTTGATCTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA 960
DB 917 TCCTTTTCTGATTTGATCTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAA 976

QY 961 CTGAGGTATGGAGCCTCCATCATCA 985
DB 977 CTGAGGTATGGAGCCTCCATCATCA 1001

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; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: F2630PIC25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.5%; Score 980.2; DB 10; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAATGAATGGCTTTGATCTTTCATCTTCTTCGAGAAACCAATTTATCTCTCTGCTACTAT 60
DB 17 CAGCAATGAATGGCTTTGATCTTTCATCTTCTTCGAGAAACCAATTTATCTCTCTGCTACTAT 76
QY 61 TTCTTTTGGCAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCT 120
DB 77 TTCTTTTGGCAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCT 136
QY 121 GTCCACACACACAATTTCCACAGGACCCCAAGGAGATGATGGTCAAAAAGAGATCCAG 180
DB 137 GTCCACACACACAATTTCCACAGGACCCCAAGGAGATGATGGTCAAAAAGAGATCCAG 196
QY 181 GAGAGGGAAGAGATGCGCAAGTGGGACGATGGGCGGCAAGGAATTAAGAGAGAC 240
DB 197 GAGAGGGAAGAGATGCGCAAGTGGGACGATGGGCGGCAAGGAATTAAGAGAGAC 256
QY 241 TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 300
DB 257 TGGGTGATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 316
QY 301 ACAAAGGGGAAAAGTTTCTTGGGAATACCTGGGAAAAGGCAAGCAGTACTGTCT 360
DB 317 ACAAAGGGGAAAAGTTTCTTGGGAATACCTGGGAAAAGGCAAGCAGTACTGTCT 376
QY 361 GTGATTCGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATGCCCCGCTCA 420
DB 377 GTGATTCGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATGCCCCGCTCA 436
QY 421 AGACATCTATGAATTTGTCAAGATGTGATAGCAGGATTTAGGAACTGAGAGAAAT 480
DB 437 AGACATCTATGAATTTGTCAAGATGTGATAGCAGGATTTAGGAACTGAGAGAAAT 496
QY 481 TCTACTCATCTGCAGGAGAGAGAACTACAGGGAATCCCTTAACCCACTCGAGATTC 540
DB 497 TCTACTCATCTGCAGGAGAGAGAACTACAGGGAATCCCTTAACCCACTCGAGATTC 556
QY 541 GGGTGAATGCTAGCATCGCCAGAGATGAAGCTGCCAACACACTCATCTGCTGATG 600
DB 557 GGGTGAATGCTAGCATCGCCAGAGATGAAGCTGCCAACACACTCATCTGCTGATG 616
QY 601 TTGCCAAGAGTGGCTTTCTTGGGTGTTCACTGGGTGATGACCTTGAAGAGGAGGAC 660
DB 617 TTGCCAAGAGTGGCTTTCTTGGGTGTTCACTGGGTGATGACCTTGAAGAGGAGGAC 676
QY 661 AGTACATGTTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAC 720
DB 677 AGTACATGTTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAC 736
QY 721 CCAGGACCCCTATGTCATGAGACTGTCTGGAGATGCTGAGCTCTGGCAGATGGAATG 780
DB 737 CCAGGACCCCTATGTCATGAGACTGTCTGGAGATGCTGAGCTCTGGCAGATGGAATG 796
QY 781 ACACAGAGTGCATCTTACCATGTACTTGTCTGTGAGTTTCATCAAGAAGAAAAGTAA 840
DB 797 ACACAGAGTGCATCTTACCATGTACTTGTCTGTGAGTTTCATCAAGAAGAAAAGTAA 856
QY 841 TTCCCTCATCTAGTATTTCTTCTTCTGTCGACCGTCAATACAGTTATTTGTTATCA 900
DB 857 TTCCCTCATCTAGTATTTCTTCTTCTGTCGACCGTCAATACAGTTATTTGTTATCA 916
QY 901 TCTTTTCTTCTGATGTTCTATCATATTGATCTGAGTCAACATAGCTAGAAAATGCTAAA 960
DB 917 TCTTTTCTTCTGATGTTCTATCATATTGATCTGAGTCAACATAGCTAGAAAATGCTAAA 976
QY 961 CTGAGGTATGAGGCTCCATCATCA 985
DB 977 CTGAGGTATGAGGCTCCATCATCA 1001

RESULT 11

US-09-999-833A-96

; Sequence 96, Application US/09999833A

; Publication No. US20030054405A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.5%; Score 980.2; DB 10; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAATGATGGCTTTGGCATCTTGGCTTCGAGAACCAATTTATCTCTCTGTTACTAT 60
Db 17 CAGCAATGATGGCTTTGGCATCTTGGCTTCGAGAACCAATTTATCTCTCTGTTACTAT 76
QY 61 TTCTTTTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTCTACCGCTGAAGTCT 120
Db 77 TTCTTTTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTCTACCGCTGAAGTCT 136
QY 121 GTGCCACACACAAATTCACGAGCCGCAAGAGATGATGTTGAAAAGGAGATCCAG 180
Db 137 GTGCCACACACAAATTCACGAGCCGCAAGAGATGATGTTGAAAAGGAGATCCAG 196
QY 181 GAGAGAGGGAAAGCATGGCAAGTGGGCGGCGCAAGGAATTAAGAGGAGAAC 240
Db 197 GAGAGAGGGAAAGCATGGCAAGTGGGCGGCGGCAAGGAATTAAGAGGAGAAC 256

QY 241 TGGGTGATATGGGAGATCGGGGCAATATTGCGAAGACTGGGCCCATTTGGGAAGAAGGGTG 300
DB 257 TGGGTGATATGGGAGATCAGGGCAATATTGCGAAGACTGGGCCCATTTGGGAAGAAGGGTG 316
QY 301 ACAAGGGGAAAAAGTTTCTTGGATACCTGGAGAAAAAGCAAGCAGGTACTGTCT 360
DB 317 ACAAGGGGAAAAAGTTTCTTGGATACCTGGAGAAAAAGCAAGCAGGTACTGTCT 376
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DB 377 GTGATTTGGGAAGATACCGGAATTTTGGCAACTTGGANATATGATTTGCCCGGTCA 436
QY 421 AGACATCTATCAAGTTTGTCAAGATCTGATACAGGATTTAGGGAACCTGAAGAGAAT 480
DB 437 AGACATCTATCAAGTTTGTCAAGATCTGATACAGGATTTAGGGAACCTGAAGAGAAT 496
QY 481 TCTACTACATCGTCCAGAGAGAGAACTACAGGAATCCCTTAACCCCACTGCAGGATTC 540
DB 497 TCTACTACATCGTCCAGAGAGAGAACTACAGGAATCCCTTAACCCCACTGCAGGATTC 556
QY 541 GGGGTGGAATCTAGCCATGCCCAAGATGAAGTCCCAACACACTCATCGCTGACTATG 600
DB 557 GGGGTGGAATCTAGCCATGCCCAAGATGAAGTCCCAACACACTCATCGCTGACTATG 616
QY 601 TTGCCAAGAGTGGCTTCTTTCCGGGTGTTTCAATGGCGTGAATGACCTTGAAGGGAGGGAC 660
DB 617 TTGCCAAGAGTGGCTTCTTTCCGGGTGTTTCAATGGCGTGAATGACCTTGAAGGGAGGGAC 676
QY 661 AGTACATGTTCCACAGACAACCTCCTCAGCACTATAGCACTGGAATGAGGGGGAC 720
DB 677 AGTACATGTTCCACAGACAACCTCCTCAGCACTATAGCACTGGAATGAGGGGGAC 736
QY 721 CCAGCGACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 780
DB 737 CCAGCGACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATG 796
QY 781 ACACAGAGTGCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAAAGTAA 840
DB 797 ACACAGAGTGCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAAAGTAA 856
QY 841 TTCCCTCATCTAGTATTGCTATTTTCTGTGACCGCTCATTCACAGTATTGTTATCCA 900
DB 857 TTCCCTCATCTAGTATTGCTATTTTCTGTGACCGCTCATTCACAGTATTGTTATCCA 916
QY 901 TCCCTTTTCTGATTTGATCTACATTTGATCTGAGTCAACATGCTAGAAATGCTAAA 960
DB 917 TCCCTTTTCTGATTTGATCTACATTTGATCTGAGTCAACATGCTAGAAATGCTAAA 976
QY 961 CTGAGGTATGAGCCTCATCATCA 985
DB 977 CTGAGGTATGAGCCTCATCATCA 1001

RESULT 12
US-09-981-915A-96
; Sequence 96, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Ruc, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Pacni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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Query Match
 Best Local Similarity 99.7%; Score 980.2; DB 10; Length 1016;
 Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	CAGCAATGAATGGCTTTGCATCCTTTCGTAAGAACAACCAATTATTCCTCCCTGGTACTAT	60
Dd	17	CAGCAATGAATGGCTTTGCATCCTTTCGTAAGAACAACCAATTATTCCTCCCTGGTACTAT	76
Qy	61	TTCCTTTTGCAAATTCAGAGTCTGGGTCTCGATATTGATACCCTCTCTCCGCTGAAGTCT	120
Dd	77	TTCCTTTTGCAAATTCAGAGTCTGGGTCTCGATATTGATACCCTCTCTA CCGCTGAAGTCT	136
Qy	121	GTCGCCACACACAAATTTCCACGAGCCCAGAGATGATGGTGAATAAAGGAGATCCAG	180
Dd	137	GTCGCCACACACAAATTTCCACGAGCCCAGAGATGATGGTGAATAAAGGAGATCCAG	196
Qy	181	GAGAGAGGGGAAGCATTGGCAAGCTGGGAGCGCATGGGGCCGAAGGAATTTAAAGGAGAAC	240
Dd	197	GAGAGAGGGGAAGCATTGGCAAGCTGGGAGCGCATGGGGCCGAAGGAATTTAAAGGAGAAC	256
Qy	241	TGGGTGATATGGGAGATCGGGCCAATATTGGCAAGACTGGGCCCATTTGGGAAGAAGGGTG	300
Dd	257	TGGGTGATATGGGAGATCAGGGCCAATATTGGCAAGACTGGGGCCCATTTGGGAAGAAGGGTG	316
Qy	301	ACAAAGGGGAAAAGGTTTGCTTGGGAATCCTGGAGAAAAAGGCAAGCAGGTACTGTCT	360
Dd	317	ACAAAGGGGAAAAGGTTTGCTTGGGAATCCTGGAGAAAAAGGCAAGCAGGTACTGTCT	376
Qy	361	GTGATTGTGGGAAGATPACCGGAAAATTGTGTGGACCAACTGGGATATTAGTATTGCCCGGCTCA	420
Dd	377	GTGATTGTGGGAAGATACCGGAAAATTGTGTGGACCAACTGGGATATTAGTATTGTCTCGGCTCA	436
Qy	421	AGACATCTATGAGATTTCGAAGAAATGTGATAGCAGGGATTAGGAAA CTGAAGAGAAAT	480
Dd	437	AGACATCTATGAGATTTCGAAGAAATGTGATAGCAGGGATTAGGAAA CTGAAGAGAAAT	496

QY 481 TCTACTACATCGTGCAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTC 540
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DB 557 GGGGTGGATGCTAGCCATGCCCAAGGATGAGCTGCCAAGACACTCATCTCCTGACTATG 616
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DB 677 AGTACATGTTTCAGACACACTCCACTCCAGACTATAGCACTGGAATGAGGGGAC 736
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DB 737 CCAGCACCCCTATGTCATGAGGAGCTGTGCGAGATCTGAGCTCTCGCAGATGGAATG 796
QY 781 ACACAGAGTGGCATCTTACCATGTACTTTCTGTGAGTTCATCAAGAGAAAAGTAAC 840
DB 797 ACACAGAGTGGCATCTTACCATGTACTTTCTGTGAGTTCATCAAGAGAAAAGTAAC 856
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QY 901 TCTTTTTCCTGATGTACTACATTTGATCTGAGTCACTAGTCAAGATAAGAAATGCTAAA 960
DB 917 TCTTTTTCCTGATGTACTACATTTGATCTGAGTCACTAGTCAAGATAAGAAATGCTAAA 976
QY 961 CTGAGTATGAGGACCTCCATCATCA 985
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RESULT 13
US-09-978-824-96
; Sequence 96, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14

; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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QY	841	TTCCCTCAT	CTCATCTAGTATTTTCCGTGTGACCGTCATTACAGTTATTCGTATCA	900
Db	857	TTCCCTCAT	CTCATCTAGTATTTTCCGTGTGACCGTCATTACAGTTATTCGTATCA	916
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RESULT 14

US-09-918-585A-96

Sequence 96, Application US/09918585A

Publication No. US20030050406A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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FILE REFERENCE: P2630P1C1

CURRENT APPLICATION NUMBER: US/09/918,585A

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085580
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023

Query Match 61.5%; Score 980.2; DB 10; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAATGAATGGCTTTGTCATCTTCTTTCGAAAGAAACCAATTTATTCCTCTGGTACTAT 60
DB 17 CAGCAATGAATGGCTTTGTCATCTTCTTTCGAAAGAAACCAATTTATTCCTCTGGTACTAT 76

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DB 77 TTCTTTTGCAAATTCAGAGTCTGGTCTGTGATATTCATAGCCCTCTACCGCTGAAGTCT 136

QY 121 GTGCCACACACAAATTCACAGGACCCAAAGAGATGATGTGAAAAGAGATCCAG 180
DB 137 GTGCCACACACAAATTCACAGGACCCAAAGAGATGATGTGAAAAGAGATCCAG 196

QY 181 GAGAAGGGGAAAGCATGGCAAACTGGGACGATGGGCGCAAGGAATTAAGAGGAAC 240
DB 197 GAGAAGGGGAAAGCATGGCAAACTGGGACGATGGGCGCAAGGAATTAAGAGGAAC 256

QY 241 TGGGTGATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 300
DB 257 TGGGTGATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTG 316

QY 301 ACAAGGGGAAAAAGTTTGTTCGAATACCTGGAGAAAGGCAAGGAGTACTGTCT 360
DB 317 ACAAGGGGAAAAAGTTTGTTCGAATACCTGGAGAAAAGGCAAGGAGTACTGTCT 376

QY 361 GTGATTGTGGAAGATACCGGAAATTTCTTGCAACTGGATATTTAGTATTCGCCGGCTCA 420
DB 377 GTGATTGTGGAAGATACCGGAAATTTCTTGCAACTGGATATTTAGTATTCGCCGGCTCA 436

QY 421 AGACATCTATGAAGTTTGTCAAGAACTGTATAGCAGGATAGGAACTGAGAGAAAT 480
DB 437 AGACATCTATGAAGTTTGTCAAGAACTGTATAGCAGGATAGGAACTGAGAGAAAT 496

QY 481 TCTACTACATCGTCAGGAAGAGAAACTACAGGAATCCCTAACCCACTGCAGGATTC 540
DB 497 TCTACTACATCGTCAGGAAGAGAAACTACAGGAATCCCTAACCCACTGCAGGATTC 556

QY 541 GGGGTGGAATCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATG 600
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QY 601 TTGCCAAGAGTGGCTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGAGGGAC 660
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QY 841 TTCCCTCATCTTACGATTTTGTATTTCTTCTGACCGTCAATACAGTTATTTGTTATCCA 900
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Qy 961 CTGAGGTATGGAGCCCTCCATCA 985
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RESULT 15

US-09-978-423A-96
; Sequence 96, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Pan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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61 PRIOR FILING DATE: 1998-05-15
62 PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.3%; Score 980.2; DB 10; Length 1016;
Best Local Similarity 99.7%; Pred. No. 4.5e-290;
Matches 982; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAATGATGCTTGCATCTTCCGAGGAAACCAATTTATCCTCTGGTACTAT 60
Db 17 CAGCAATGATGCTTGCATCTTCCGAGGAAACCAATTTATCCTCTGGTACTAT 76
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Db 77 TTCCTTTGCAAAATTCAGAGTCTGGGTCCTGGATATTGATAGCGGTCCTACCGCTCAAGTCT 136
Qy 121 GTGCCACACACACAAATTTCCACAGGACCCCAAGGAGATGATGGTGAAGAGAGATCCAG 180
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Qy 481 TCTACTACATCGTCGAGAGAGAGAACTACAGGGAATCCCTACCCACTCGCAGGATTC 540
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Qy 781 ACACAGAGTCCCATCTTACCATGATCTTTGCTGTGAGTTCATCAAGAGAAAAAGTAAC 840
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